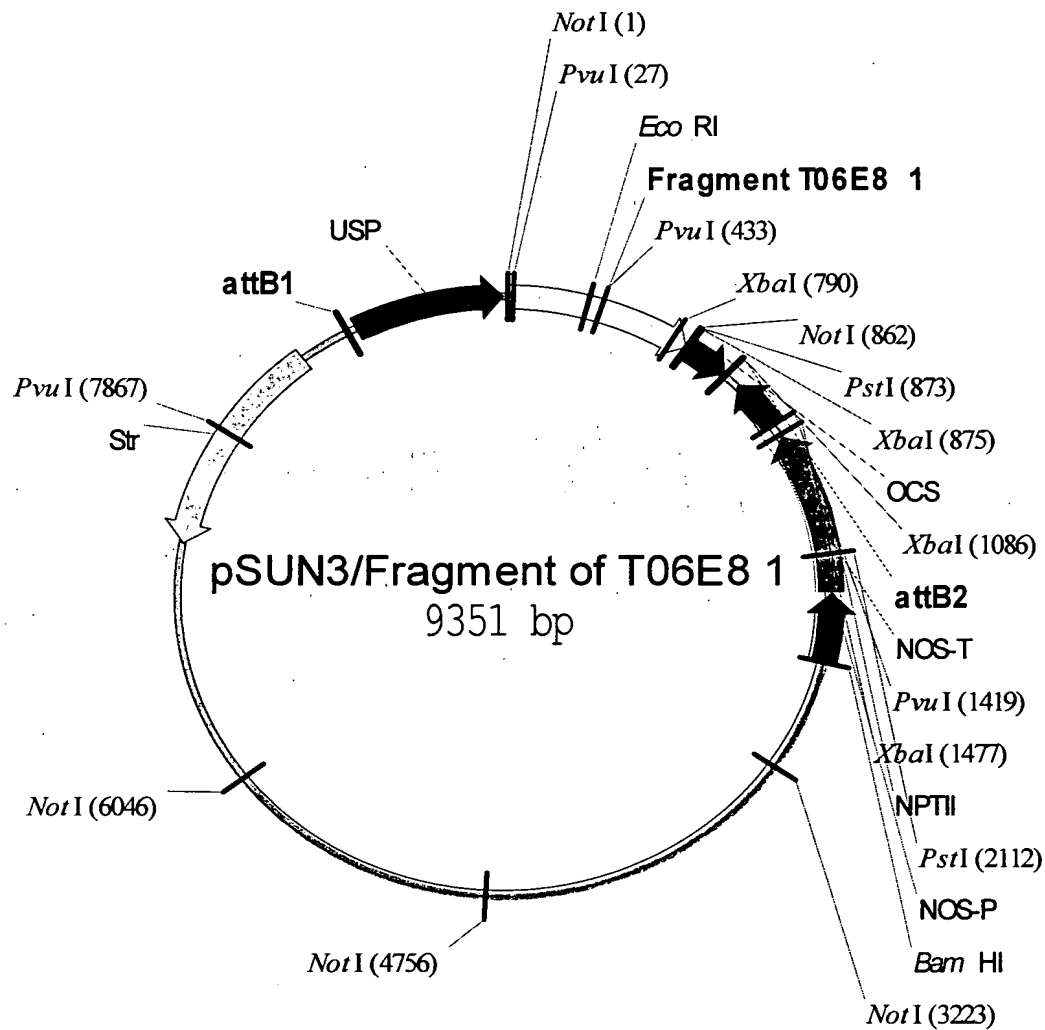


Figure 1: Vector map of pSUN3CeLPLAT



BEST AVAILABLE COPY

Figure 2: Amino acid sequence alignment of *C. elegans* LPLATs (Ce-T06E8.1 and Ce-F59F4.4) with the *M. musculus* LPAAT (Mm-NP061350).

```

1                                     50
Mm-NP061350 MELWPGAWTA LLLLLELLLS TLWFCSSSAK YEFKMAEYNG WELFLAILAI
Ce-T06E8.1  ...MENFWSI VVFFLESIIF ILYNISTVCH YMYRISEYF TILLHGMEVC
Ce-F59F4.4  .....MTF LAILEFVIAVL LLLAQLPVIG FYIRAVYEGM CLLIGGFLGG

51                                     100
Mm-NP061350 PVC AVRGRNV ENMKIERLL LHAKYLYGER VEVGAHHFP PTQPYVVVSN
Ce-T06E8.1  VTMIPSWLNG KGADYMFHSF FYWCKWTGVH TTVYGYEKTQ VEGPAVAVCN
Ce-F59F4.4  LASIPFGKSP NNHFRMFKIF QAMTWPMGVR FELRNSEILH DKKPYITLHAN

101                                    150
Mm-NP061350 HQSSLDLGLM MEVLPRDCVP IAKRELLWAG SAGLACWLAG TTEIDRKRRTG
Ce-T06E8.1  HQSSLDLGLM ASIWPKNQCV MMKRILAVVP FFNLGAYFSN TTEIDRYNRE
Ce-F59F4.4  HQSALDVLGM SFAWPVDCV MLKSSLKMLP GFNLCAVLC D SVYINRFSKE

151                                    200
Mm-NP061350 DATSVMSEVA QTILTDQVRV WVFPEGTRNH NGSMIPFKRG AFHLAVQAQV
Ce-T06E8.1  RAMASVDYCA SEMKNRNLKI WVFPEGTRNR EGGFIPFKKG AFNIAVRAQI
Ce-F59F4.4  KALKTVDTTL HEIVTKKRKV WLYPEGTRNA EPELLPFKKG AFILAKQAKI

201                                    250
Mm-NP061350 PIIPIVMSSY QDFYSKKERR FTSPGRCQVR VLPPVSTEGL TPDDVPALAD
Ce-T06E8.1  PIIPVVFSDY RDFYSKPGRY FKNDGEVVIR VLDAIPKGL TLDDVSELS D
Ce-F59F4.4  PIVPCVFSSH KFFYSHAEKR LTS.GNCILD ILPEVDSS.. KFD SIDDLSA

251                                    285
Mm-NP061350 SVRHSMLTIF RETSTDGLGG GDCLKKPGGA GEARL
Ce-T06E8.1  MCRDVMLAAY KEVTLEAQR NATRRGETKD GKKSE
Ce-F59F4.4  HCRKIMQHR EKIDAEANL NI.....

```

3/37

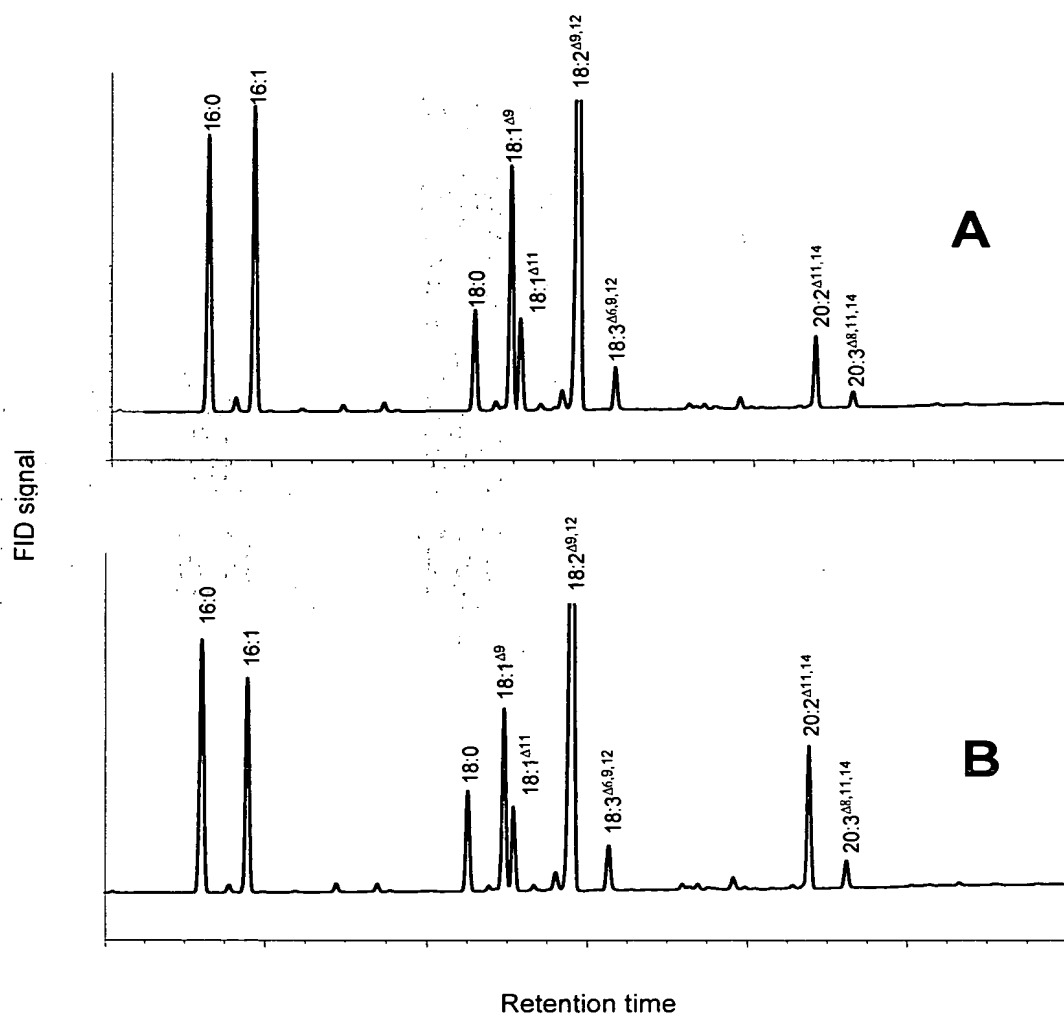
Figure 3: Fatty acid profiles of transgenic C13ABYS86 *S. cerevisiae* cells

Figure 4: Elongation of exogenously applied $18:2^{\Delta 9,12}$ and $18:3^{\Delta 9,12,15}$, respectively, following their endogenous Δ -6-desaturation (data from figs 2 and 3).

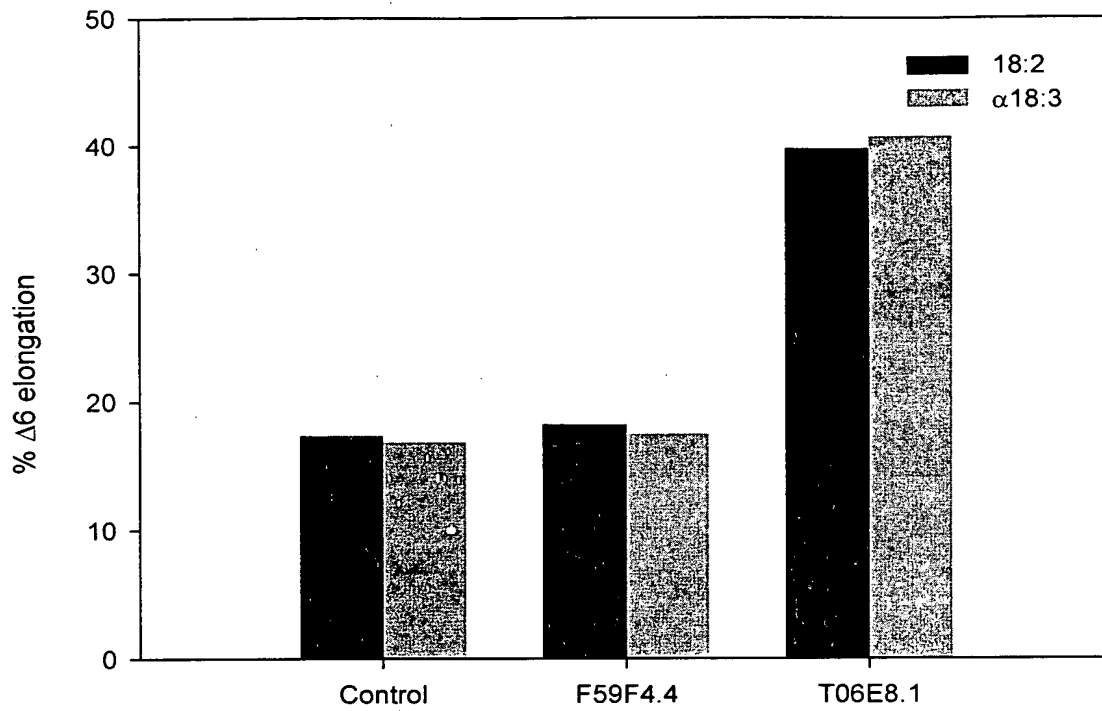


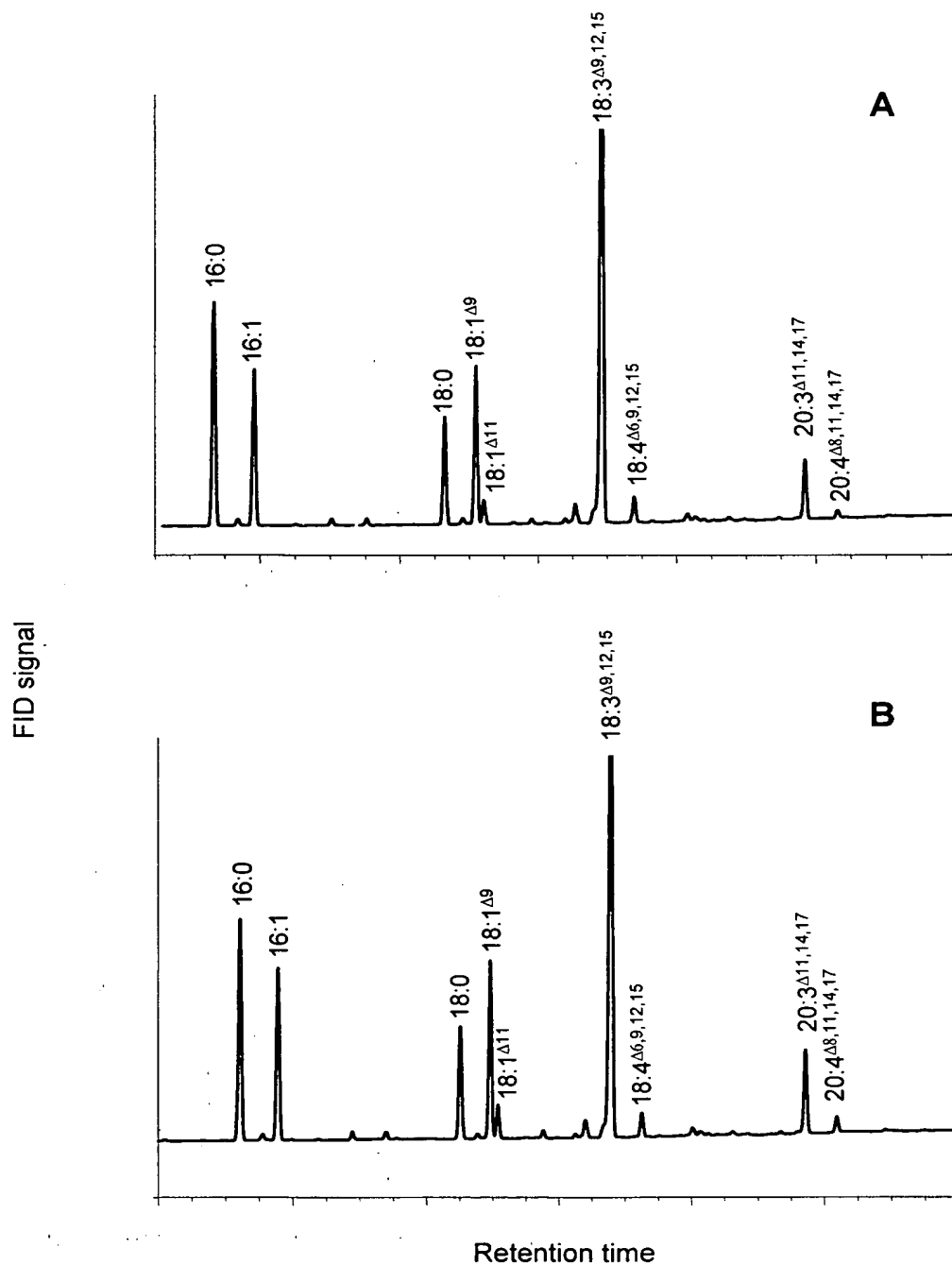
Figure 5: Fatty acid profiles of transgenic C13ABYS86 *S. cerevisiae* cells

Figure 6: Acyl-CoA composition of transgenic INVSc1 yeasts which had been transformed with the vectors pESCLeu PpD6Pse1/pYes2 (A) or pESCLeu-PpD6-Pse1/pYes2-T06E8.1 (B).

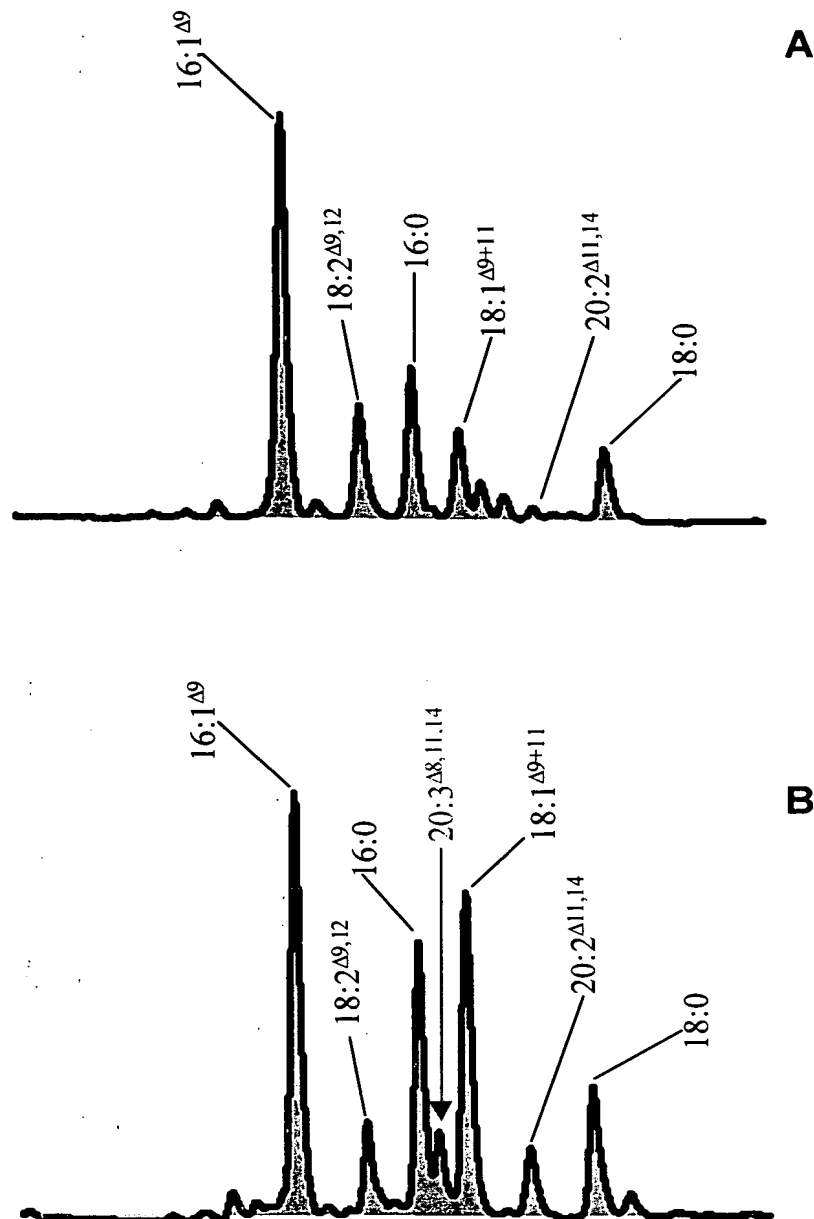


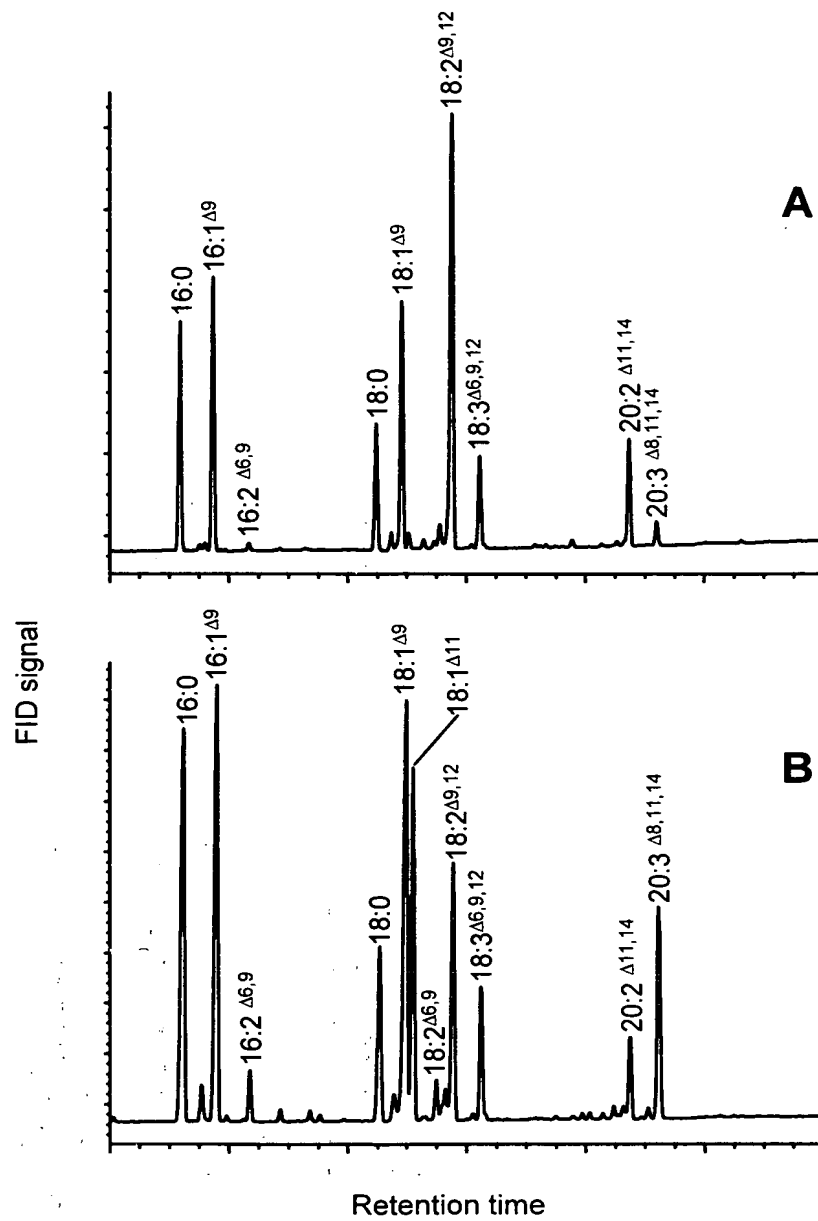
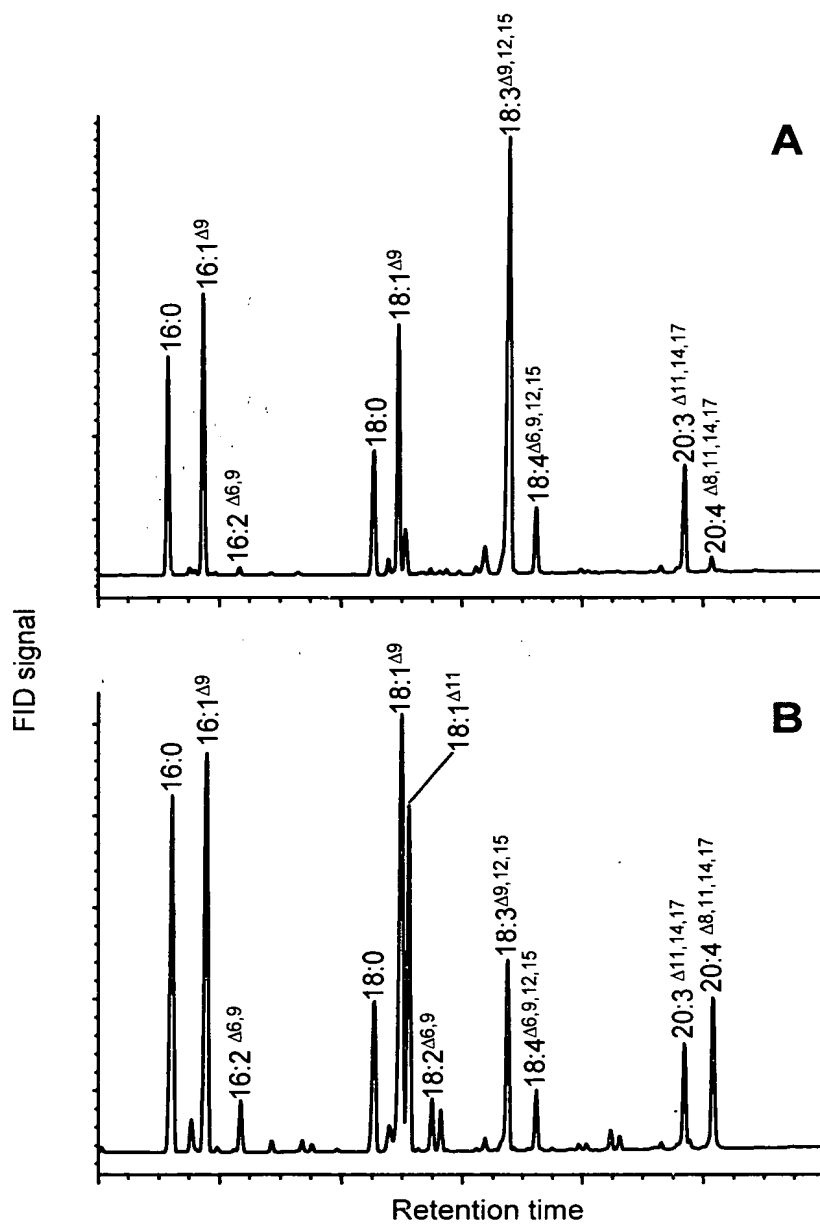
Figure 7: Fatty acid profiles of transgenic INVSc1 *S. cerevisiae* cells

Figure 8: Fatty acid profiles of transgenic INVSc1 *S. cerevisiae* cells.

9/37

Figure 9A: Vector map of pGPTV LeB4-700 + T06E8.1

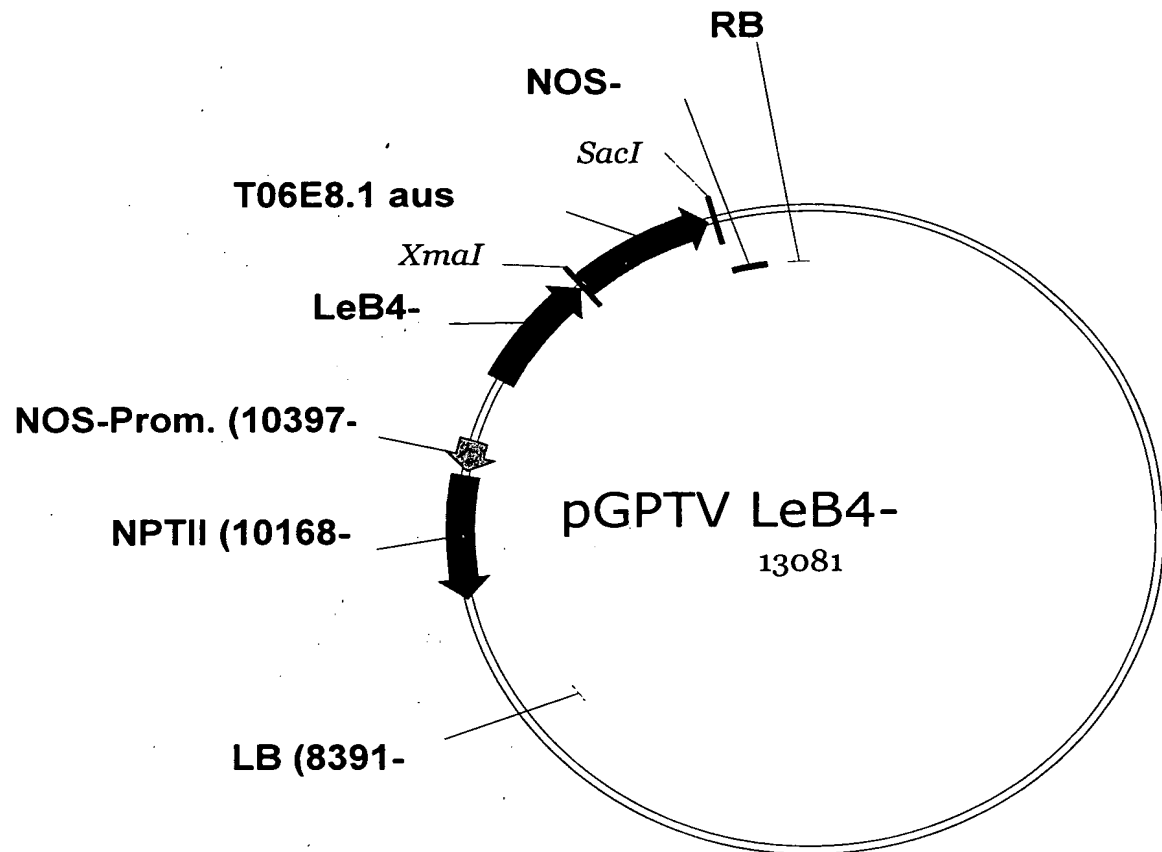
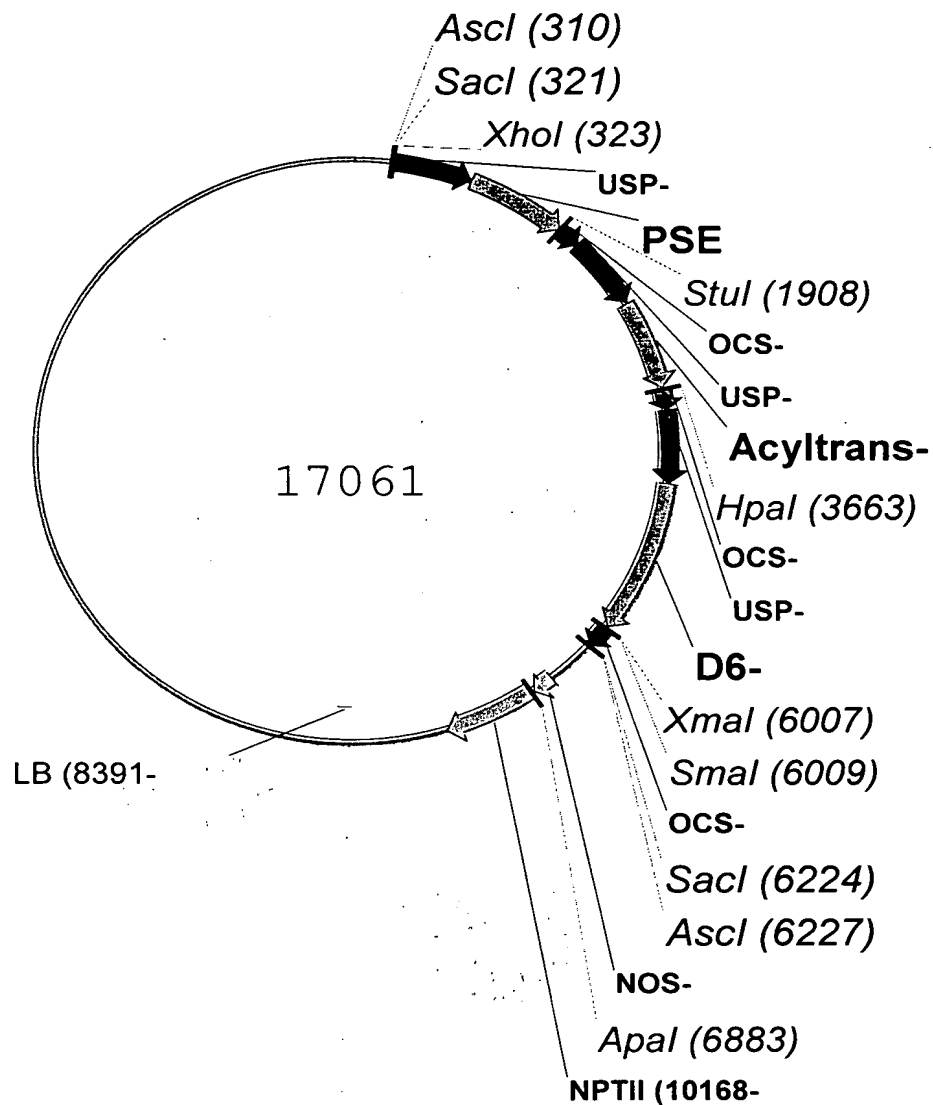


Figure 9B: Vector map of pGPTV USP/OCS-1,2,3 PSE1(Pp)+D6-Des(Pt)+2AT (T06E8-1)

pGPTV/USP/OCS-1,2,3 PSE1(Pp) D6-Des(Pt)-2 AT(T06E8-1)



11/37

Figure 10A: Biosynthetic pathway of LCPUFAs

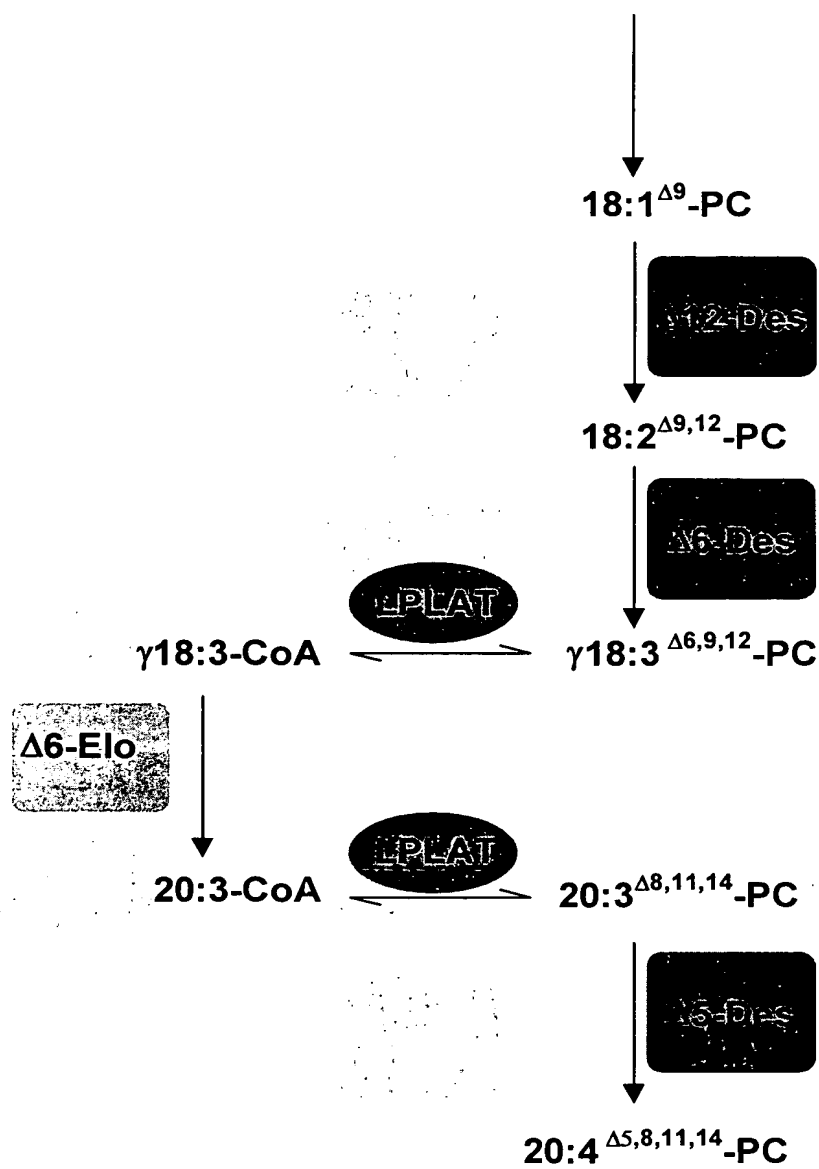


Figure 10B: Biosynthetic pathway of LCPUFAs

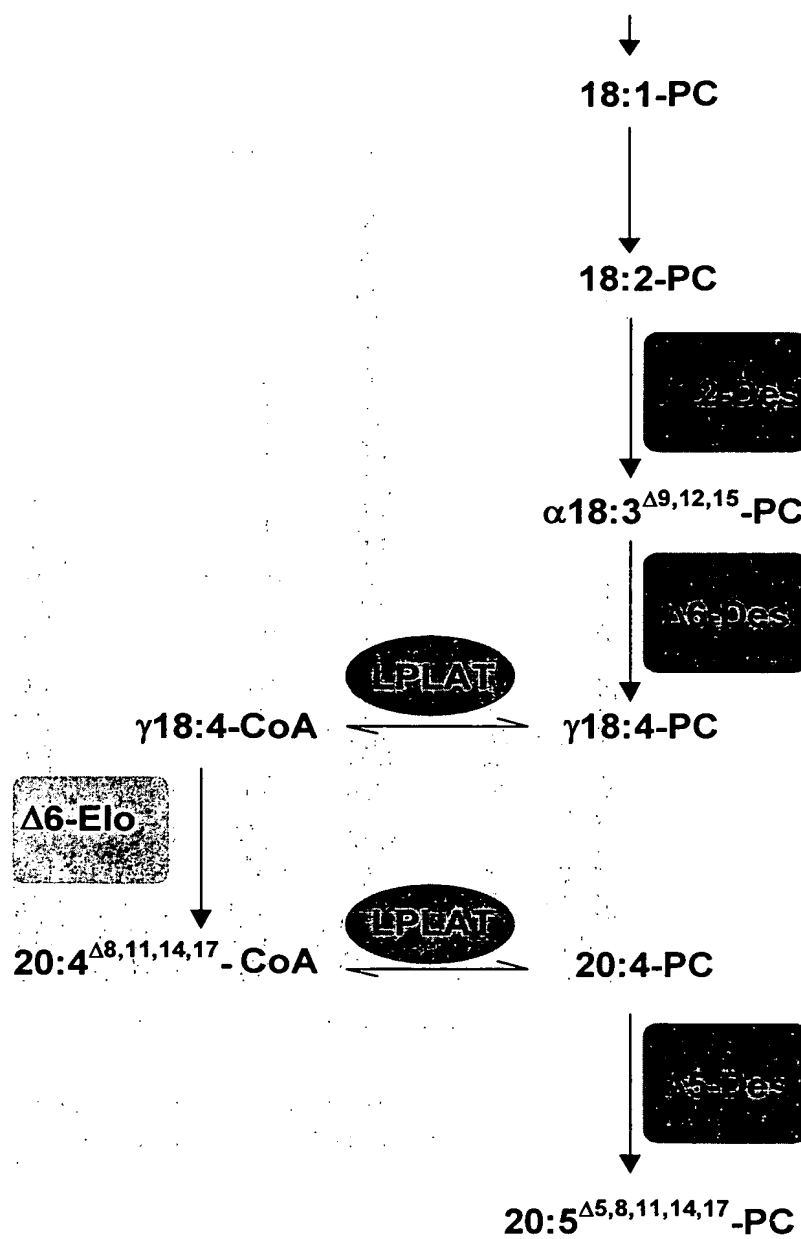


Figure 11: Comparison of GPAT and LPAAT substrate specificities in linseed, sunflower and *Mortierella alpina*

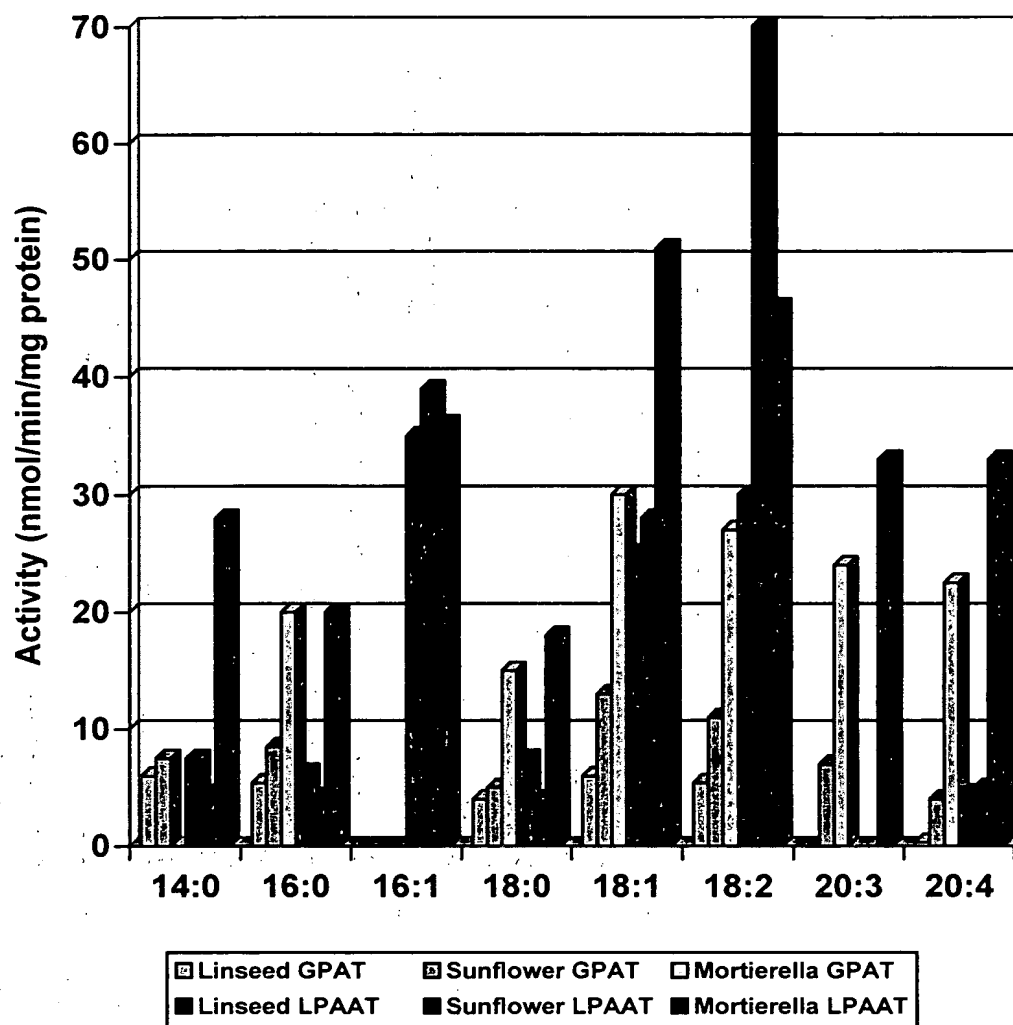
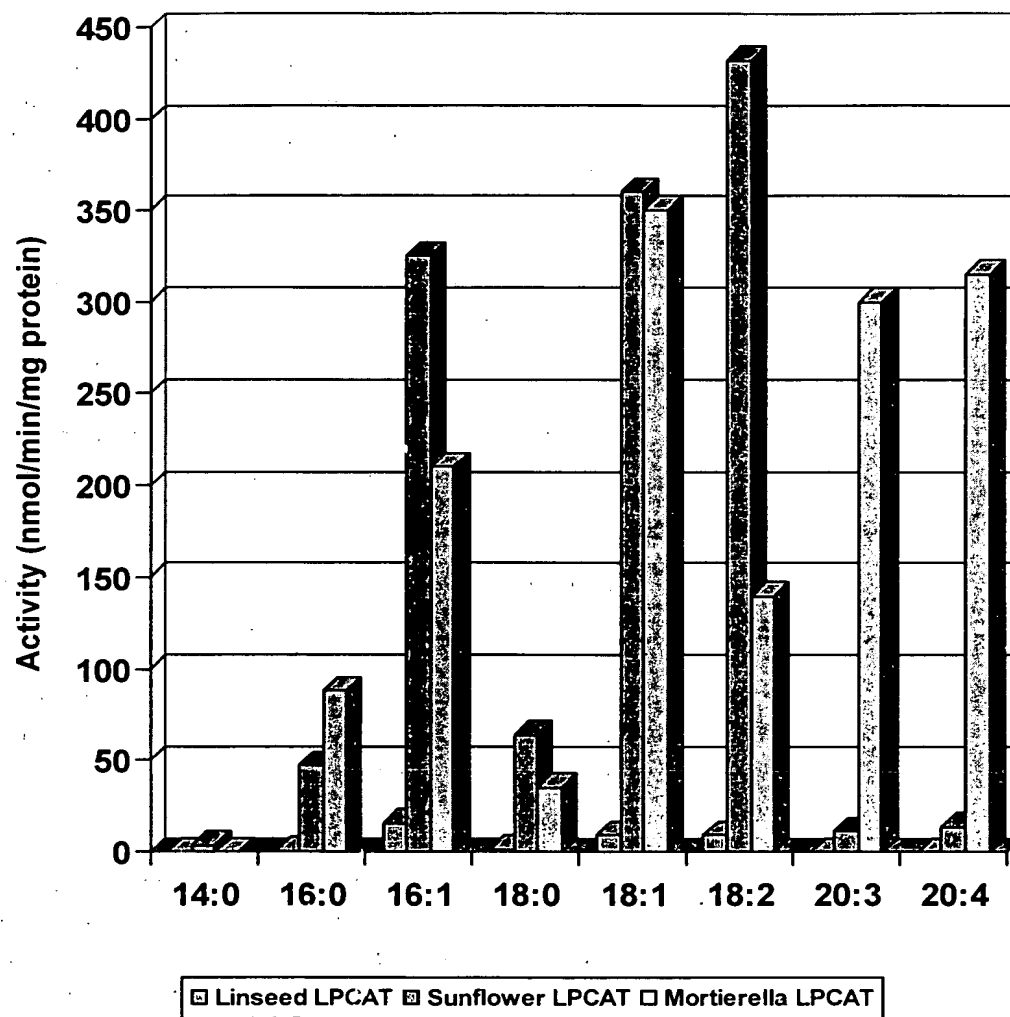


Figure 12: Comparison of LPCAT substrate specificity in linseed, sunflower and -
Mortierella alpina



15/37

Figure 13: Alignment of SEQ ID NO: 2 with Swiss Prot database

	1	50
Q9JZ47	MSSNKASFFTRL
Q9JU41	MSSNKASFFTRL
Q59601	MSSNKASFFTRL
Q9HW50	MARLRLLLR SARL
SEQ ID NO: 2	MSAWTRAKTAVGL
O35259		METIMDDEVTKRTSAEELESWNLLSRTNYNFQYISLRLTILWGLGVLI RY
	51	100
Q9JZ47	RRLCRLAVWLFKTKGNLRGIDGG.CPESRNRAVIELGRGVLAALD.....	
Q9JU41	RRLCRLTVWLFKTKGNLRGIDGG.CPESRNRAVIELGRGVLAALD.....	
Q59601	RRLCRLTVWLFKTKGNLRGIDGG.CPKSRNRAVIALGKGALAALD.....	
Q9HW50	LGLVALGLGLAAWVSLRERLPGADVTPLRQRLTRWWLARLCAALP.....	
SEQ ID NO: 2	LTLAPARIVFLVTVLGTYGLTVAACRLGVPKSFVLGLTRCVARLTLWGL	
O35259	CFLPLRIALAFTGIGLLVVGTTMVGYPNGRFKEFLSKHVHLMCYRICV	
	101	150
Q9JZ47	..IGLEVGRPAPEHPNG..VLVAANHVS WLDIFAMS.AVYPSSFIAKQEI	
Q9JU41	..IGLEVGRPAPEHPNG..VLVAANHVS WLDIFAMS.AVYPSSFIAKQEI	
Q59601	..IGLEVGRPAPEHPNG..VLVAANHVS WLDIFAMS.AVYPSSFIAKQEI	
Q9HW50	..FEVRVSGEAPRQP...MLWVANHVSWTDIPLLG.ALAPLTFLSKA EV	
SEQ ID NO: 2	GFYHIEVSCDAQGLREWP.RVIVANHVSYLEILYFMSTVHCP SFVMKKTC	
O35259	RALTAIITYHNRKNRPRNGGICVANHTSRIDV IIFASDGYAMVGQVHGG	
	151	200
Q9JZ47	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q9JU41	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q59601	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q9HW50	RAWPLAGWLAEKAGTLFIRRGSG.....DSRLINQRLAEQLHRGR	
SEQ ID NO: 2	LRVPLVGYIAMELGGVIVDREGGQSASAIIRD RVQEPPRDSSEKHHAQ	
O35259	LMGVIQRAMVKACPHVWFERSEVK.....DRHLVAKRLTEHVQDKS	
	201	250
Q9JZ47	..NVSFFPEARTSSGLGLLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q9JU41	..NVSFFPEARTSSGLGLLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q59601	..NVSFFPEARTSSGLGLLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q9HW50	..NLLIFPEGTTTNGESLRTFHGRLMASALEAGVAVQPVAISYRRDGV PD	
SEQ ID NO: 2	..PLLVFPEGTTTNGSCLLQFKTGAFR...PG.APVLPVVLEFPIDKARG	
O35259	KLPILIFPEGTCINNTSVMMFKKGSFEIG...ATVYPVAIKY..DPQFG	

16/37

	251	300
Q9JZ47	TARPSYADVGLPTCLWRIVSMKKLTIRVDFVCVADAAE.....	
Q9JU41	TARPSYADVGLPTCLWRIVSMKKLTIKVDFVCVADAAE.....	
Q59601	TARPSYADVGLPTCLWRIVSMKKLTIKVDFVCVADAAE.....	
Q9HW50	AQAPFIGDDDLLSHLGRLLRGERGSVHIQLLEPIPSQ.....	
SEQ ID NO: 2	DFSPAYESVHTPAHLLRMLAQWRHRLRVRYLPLYEPSAAEKVDADLYARN	
O35259	DAFWNSSKYGMVTYLLRMMTSAIVCSVWYLPMTRE.....	

	301	349
Q9JZ47	...SEDRYALKDKIEESIRAVVADDADIIV.....	
Q9JU41	...SEDRYALKDKIEESIRAVVADDADIIV.....	
Q59601	...SEDRYALKDKIEESIRAVVADDADIIV.....	
Q9HW50	...GLDRAELARQAQQAVRLALFGTAAPTQTRRAA.....	
SEQ ID NO: 2	VRDEMARALKVPTVEQSYRDKLVYHADLMPHYQKAGPGALYLYVRPDL	
O35259KDEDAVQFANRVKSAIARQEDW.....	

17/37

Figure 14: Alignment of SEQ ID NO: 5 with Swiss Prot database

	1	50
Q9C9P8	MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLLYFAPIAALG	
Q9SFJ1	MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLLYFAPIAALG	
Q9LHN4MEKKSVPNSDKLSLIRVLRGIIICLMVLVSTAFMMLIFWGFLSAVV	
SEQ ID NO: 5	
Q9SDN3	
Q9XFW4MAMAAVIVPLGILFFISGLVVNLLQAVCYVLV	
	51	100
Q9C9P8	LRLLSVQQSRKVVSLLIFGLWLALWPYLFETVNGTTVVFSGDIIP...VEK	
Q9SFJ1	LRLLSVQQSRKVVSLLIFGLWLALWPYLFETVNGTTVVFSGDIIP...VEK	
Q9LHN4	LRLFSIRYSRKCVSFFFGSWLALWPFLFEKINKTKVIFSGDKVP...CED	
SEQ ID NO: 5MDVVKVIFAGDKVP...KEN	
Q9SDN3MGKE	
Q9XFW4	RPMSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQVFADDETFRNMKE	
	101	150
Q9C9P8	RVLLIANHRTEVDWMYLWNIALRKGCGLGYIKYVLKSSLMKLPFIGWGPHV	
Q9SFJ1	RVLLIANHRTEVDWMYLWNIALRKGCGLGYIKYVLKSSLMKLPFIGWGPHV	
Q9LHN4	RVLLIANHRTEVDWMYFWDLALRKQIGNIKYVLKSSLMKLPFIGWAFHL	
SEQ ID NO: 5	RVMVMCNHRTEVDWMIWNLAIRKKGKIGYCKYAVKNSVKNLPLFGWAFYV	
Q9SDN3	HALVISNHRSDIDWLVGWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWF	
Q9XFW4	HALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWF	
	151	200
Q9C9P8	LEFIPVERKREVDEPVLLQMLSSFKDPQEPLWLALFPEGTDFTTECKRS	
Q9SFJ1	LEFIPVERKREVDEPVLLQMLSSFKDPQEPLWLALFPEGTDFTTECKRS	
Q9LHN4	FEFIPVERRWEVDEANLRQIVSSFKDPRDALWLALFPEGTDYTEACKQRS	
SEQ ID NO: 5	FEFLMLHRKWEVDAPVIKTYIDSFQDKRDPLWLVVFPPEGTDFTSEAKRDTG	
Q9SDN3	SEYLFLEERSWAKDEGTLKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAA	
Q9XFW4	SEYLFLEERNWAKDESTLQSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAA	
	201	250
Q9C9P8	QKFAAEVGLPALSNVLLPKTRGFGVCLEVLHNSLDAVYDLTIAYKPRCP.	
Q9SFJ1	QKFAAEVGLPALSNVLLPKTRGFGVCLEVLHNSLDAVYDLTIAYKPRCP.	
Q9LHN4	KKFAAENGLPILNNVLLPRTKGFSCLQELSCSLDAVYDVTIGYKTRCP.	
SEQ ID NO: 5	NAIGREKGYPELVNVLQPRTRGFTVCLSQSRCSLDAVYDLTIAYKPRCP.	
Q9SDN3	QEYAAATGLPVPRNVLIPTKGFVTAVSQMRSFAPAIYDVTVAIPKSSPA	
Q9XFW4	QEYAASELFPVPRNVLIPTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPP	

18/37

	251	300
Q9C9P8	SFMDNVFGTDPSEVHIHVRRVLLKEIPANEAESSAWLMDSFKLKDKLSD	
Q9SFJ1	SFMDNVFGTDPSEVHIHVRRVLLKEIPANEAESSAWLMDSFKLKDKLSD	
Q9LHN4	SFLDNVYGI EPSEVHIHRRINLTQIPNQEKDINAWLMNTFQLKDQLLND	
SEQ ID NO: 5	LFINN VFGTDPSEVHIHRRIPISEIPQSEDGMTQWLYDLFYQKDQMLAS	
Q9SDN3	PTMLRRLFEGRPSVVHVHIKRHV MRDL PETDEAVAQWCKDIFVAKDALLDK	
Q9XFW4	PTMLRRLFKGQPSVVHVHIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDK	

	301	350
Q9C9P8	FNAQGKFPNQRPEEELSVLKCIATFAGKQQQVTKPSCQKVFLLLNQSSDE	
Q9SFJ1	FNAQGKFPNQRPEEELSVLKCIATFAGKQQQVTKPSCQKVFLLLNQSSDE	
Q9LHN4	FYSNGHFPNEGTEKEFN TKYLINCLAVIAFTTICTHLTFFSSMIWFRIY	
SEQ ID NO: 5	FSKTGSFPDSGIE.ESPLNIVEGVCNVALHVVL SGWVFWCLFHSVWLKLY	
Q9SDN3	HTVEQTFGDQQLKVTGRPLKSLLVVTAWACLLILGALKFLYWSSLLSSWK	
Q9XFW4	HIAADTFPGQKEQNIGRPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWK	

	351	400
Q9C9P8	KESKKAVAQHPFTDTLDHLFQVEHSISCFLYMHYINLSTCHLISLYE...	
Q9SFJ1	KESKKAVAQHPFTDTLDHLFQVEHSISCFLYMHYINLSTCHLISLYE...	
Q9LHN4	VSLACVYLTSATHFNLR SVPLVETAKNSLKL VNK.....	
SEQ ID NO: 5	VAFASLLAFSTYFDWRPKPVYSSLRTRKIV.....	
Q9SDN3	GIAFSALGLGVVTVLMQILIRFSQSERSTPAPVAPTNNKNKGESSGKPEK	
Q9XFW4	GIALSAFGLGIITLCMQILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQT	

	401
Q9C9P8
Q9SFJ1
Q9LHN4
SEQ ID NO: 5
Q9SDN3	QQ.....
Q9XFW4	EVEEKQK

19/37

Figure 15: Alignment of SEQ ID NO: 35 with Swiss Prot database

	1	50
P04180	MGP
Q08758	MGP
Q9MZ04	MGL
Q9DDJ6	MGR
Q9Y2B3	MGL
SEQ ID NO: 35	MCSISCGSTPQQLC	HYRKS
	51	100
P04180	PGSPWQWVTL	LLG
Q08758	PGSPWQWVPL	LLG
Q9MZ04	PGSPWQWVLL	LLLE
Q9DDJ6	TGAGFALLT	LLLL
Q9Y2B3	HLRPYRVGL	LP
SEQ ID NO: 35	SSSQFFIVVL	TLTL
	101	150
P04180	AELSNHTRPV	ILV
Q08758	AELSNHTRPV	ILV
Q9MZ04	AELSNHTRPV	ILV
Q9DDJ6	APPTNSTP	FPV
Q9Y2B3	...AGRHP	VPV
SEQ ID NO: 35	ARNKHHLAP	VVIV
	151	200
P04180	NMFLPLGVDC	WIDN
Q08758	NMFLPLGVDC	WIDN
Q9MZ04	NMFLPLGVDC	WIDN
Q9DDJ6	NTFLPVG	VDC
Q9Y2B3	ELLLPVI	IDC
SEQ ID NO: 35	KTLFPPFT	TCF
	201	250
P04180	SK..LAGYL	HTLV
Q08758	SK..LAGYL	HTLV
Q9MZ04	SK..LAGYM	HTLV
Q9DDJ6	SK..LAGYL	HTLV
Q9Y2B3	SKSSVGS	YFHT
SEQ ID NO: 35	SLKFLTGY	MIHL

20/37

	251	300
P04180	RKLAGLVEEMHAAYG.KPVFLIGHSLGCLHLLYFLLRQPQAWKDRFIDGF	
Q08758	HKLAGLVEEMHAAYG.KPVFLIGHSLGCLHLLYFLLRQPQAWKDRFIDGF	
Q9MZ04	RDLARLVEEMHATYG.KPVFLIGHSLGCLHLLHFLHQPQSWKDRFIDGF	
Q9DDJ6	QNLKALIEEMHDEYQ.QRVFLIAHSMGNLNVLYFLLQQRQAWKDQYIGGF	
Q9Y2B3	LALREMIEMYQLYG.GPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAF	
SEQ ID NO: 35	KDLKDLIETAYSVNANEPVVILAHSMGGLWTLFFLNQQSMEWRNKYVSRF	
	301	350
P04180	ISLGAPWGGSIKPMLVLASGDNQGIPIIMSSIKLKEEQRITTTSPWMFPSPR	
Q08758	ISLGAPWGGSIKPMLVLASGDNQGIPIIMSSIKLKEEQRITTTSPWMFPSPR	
Q9MZ04	ISLGAPWGGSIKPMQVLASGDNQGIPIIMSSIKLKEEQRITTTSPWMFPSS	
Q9DDJ6	ISLGAPWGGSVKPLRVLASGDNQGIPLMSNIKLREEQRMTTTSPWMFPTS	
Q9Y2B3	VSLGAPWGGVAKTLRVLASGDNNRIPVIGPLKIREQQRSAVSTSWLLPYN	
SEQ ID NO: 35	VSVATPWGGAVEQMMTFASGNPEGVPFVNSLVVREEQRRSESNLWLLPVR	
	351	400
P04180	MAWPEDHVFISTFSFNYTGRDFQRFADLHFEEGWYMWLQ.SRDLLAGLP	
Q08758	LAWPEDHVFISTFSFNYTGRDFQRFADLHFEEGWYMWLQ.SRDLLAGLP	
Q9MZ04	EVWPEDHVFISTFSFNYTIRDYQRFVDVHFEEGWYMWLQ.SRDLLAGLP	
Q9DDJ6	LAWPEDHIFISTPSYNYTYRDYKQFFTDVNLEDGWYMWED.MKDLLKGLP	
Q9Y2B3	YTWSPEKVVFVQTPNTINYTLRDYRKFQDIGFEDGWLMRQD.TEGLVEATM	
SEQ ID NO: 35	RCFR.DRPLVITSSRNYTAGDMEQFLCDIGFPEGVAPYKSRIPLTDILQ	
	401	450
P04180	APGVEVYCLYGVLPTPRTYIYDHGFPHYTDVPVGLYEDGDDTVATRST.E	
Q08758	APGVEVYCLYGVLPTPRTYIYDHGFPHYTDVPDVLVYEDGDDTVATRST.E	
Q9MZ04	APGVEVYCLYGVLPTPSTYIYDHDFPHYTDPLDVLYEDGDNTVATRSME	
Q9DDJ6	PPGVDTYCLYGTGYPTVETIYIYDEHFPYEDPVDMIYGDGDDTVNRRSS.E	
Q9Y2B3	PPGVQLHCLYGTGVPTPDSFYYES.FPDRDPK.ICFGDGDGTVNLSA.L	
SEQ ID NO: 35	PPQVPVTLIHGYGVPTAETLSYEK.KGFDNHPEITEGDGDGTVNVCSLTA	
	451	500
P04180	LCGLWQGRQPQPVHLLPLHGIQHLNMVFSNLTLEHINAILLGAYRQGPPA	
Q08758	LCGLWQGRQPQPVHLLPLRGIQHLNMVFSNQTLEHINAILLGAYRQGPPA	
Q9MZ04	LCSQWQGRQPQPVHLLPLHRIQHLNMVFSNQTLEHINDILLGAYRHGNPV	
Q9DDJ6	LCKRWRNQKQKVHIQELRGIDHLNMVFSNLTSSINEILLGSSQVGAGT	
Q9Y2B3	QCQAWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG.....	
SEQ ID NO: 35	VVEEWERVAGQELMIALHGKQHMQLHDDHSVQVIVDAILNVTPQEQLM	
	501	524
P04180	SPTASPEPPPPPE.....	
Q08758	SLTASPEPPPPPE.....	
Q9MZ04	PPAASPRPLTPE.....	
Q9DDJ6	KEHGELGQMGALKSSLEAGRRGKN	
Q9Y2B3	
SEQ ID NO: 35	FH.....	

21/37

Figure 16: Alignment of SEQ ID NO: 23 with Swiss Prot database

	1	50
P10349	
Q9FEP9MFILSSSSSTLPSAPPFSSSTTSIFLSFSRVSLPPSSSSSLK...	
Q39639	MFILSAVSSSSSSSSSVPSLPPFSLSPSISLSFSRVSLPPSSSSSSSSSL	
Q9FEQ0MFILSSSSSLPSPLSLSSSRVSLPPPSSSSSLN..	
Q9M4V1MLVPSALPRVSRVSAAARFSVSGVGSSPALSSRS	
SEQ ID NO: 23MPSLFRAKRNGRRTPGNAVTN...	
	51	100
P10349MAELIQDKESAQSAATAAAAS	
Q9FEP9	..LLPLSLQFGPPKLAS.SCSLRFSASRAMAELIQDKESAQSAATAAAAS	
Q39639	KLFLPLSLHFTPPKLSSPHSFLRFSASRAMAELIQDKESAHTPSTTDVTR	
Q9FEQ0	..LLPLSPHFQPPNLAC...SCSVASRSTAELLHDFKHSHTAASADEAR	
Q9M4V1	CTSLDSSVRSSLRRCPCGIYTSRTKAVVEAVESKASAREWRSVAVKRAVLA	
SEQ ID NO: 23FGKSEFH.....R..EIS...GSTRATTQVAEATTAGLRE	
	101	150
P10349	SGYERRNEPAHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQ	
Q9FEP9	SGYERRNEPAHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQ	
Q39639	N.....DPPHSRAFLDLRSEEELLSCIRRETEAGKLPSNVAAGMEELYQ	
Q9FEQ0	N.....HLPHSRAFLDVRSEQELLSYIRREAEAGKLPSNVAAGMEELYQ	
Q9M4V1	SDTGAEEEVGHSRSFLRARSEEELLSYIRKEVETGRLSSDIANGLEELYY	
SEQ ID NO: 23	TIEDRAIDGHSHSFEGIQSEEELMQVIEKEVESGRLPKRAGAGMVELYR	
	151	200
P10349	NYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSSHHKAIREPF	
Q9FEP9	NYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSSHHKAIREPF	
Q39639	NYKNAVFESGNPKADEIVLSNMTVALDRILLDVEDPFMFSPHHKAIREPF	
Q9FEQ0	NYKNAVLKSGNPKADEIVLSNMTVALDRILLDVEEPPVFSPHHKAVREPF	
Q9M4V1	NYRNAVLQSGDPRANKIILSNMAVAFDRILLDVEDPFTFSPHHQAIREPF	
SEQ ID NO: 23	NYRDAVVSSGVENAMDIVVKVMSTVLDRILLQFEEPFTFGSHHKRMVEPY	
	201	250
P10349	DYYIFGQNYIRPLIDFGNSFVGNLFLFKDIEEKLQQGHNVVLISNHQTEA	
Q9FEP9	DYYIFGQNYIRPLIDFGNSFVGNLFLFKDIEEKLQQGHNVVLISNHQTEA	
Q39639	DYYTFGQNYVRPLIDFGNSFVGNLFLFKDIEEKLHQQGHNVVLISNHQTEA	
Q9FEQ0	DYYTFGQNYVRPLIDFGNSFVGNPFLFKDIEEKLHQQGHNVVLISNHQTEA	
Q9M4V1	DYYMFGQNYIRPLIDFRSYIGNISIFSDMEEKLQQGHNIVLMSNHQTEA	
SEQ ID NO: 23	DYYTFGQNYVRPLLDFRNSYLGNLKIFDQIEKNLKEGHNVIFLSNHQTEA	

22/37

	251	300
P10349	DPAIISLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLICVYSKK	
Q9FEP9	DPAIISLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLICVYSKK	
Q39639	DPAIISLLEKTNPYIAENMIYVAGDRVIADPLCKPFSIGRNLICVYSKK	
Q9FEQ0	DPAIISLLEKTSPIYAENMIYVAGDRVIVDPLCKPFSIGRNLICVYSKK	
Q9M4V1	DPAIIALLLERTNSHIAETMVVAGDRVLTDPCKPFSMGRNLLCVYSKK	
SEQ ID NO: 23	DPAVMALLLEHSHPYLAENLTIVAGDRVLDPFCKPFSMGRNLLCVYSKK	

	301	350
P10349	HMFDIPELTETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
Q9FEP9	HMFDIPELTETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
Q39639	HMLDIPELAETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
Q9FEQ0	HMFDIPELAETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSSG	
Q9M4V1	HMDDVPELIEMKRRANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
SEQ ID NO: 23	HIHDVPDLAEMKIKANAKTLRQMTILLRQGGQYGG.....	

	351	400
P10349	EWYPAPFDASSVDNMRRLIQHSDVPGHLFPLALLCHDIMPPPSQVEIEIG	
Q9FEP9	EWYPAPFDASSVDNMRRLIQHSDVPGHLFPLALLCHDIMPPPSQVEIEIG	
Q39639	EWYPAPFDASSVDNMRRLLQHSGAPGHLYPLALLCYDIMPPPSQVEIEIG	
Q9FEQ0	EWLPAPFDASSMDNMRRLIQHSGVPGHLCPLALLCYDIMPPPSQVEIEIG	
Q9M4V1	EWHPAPFDVSSVDNMRRLEHSSVPGHIYPLSLLCYEVMPPPPQVEKQIG	
SEQ ID NO: 23	

	401	450
P10349	EKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVREAYSKALFDSVAMQYN	
Q9FEP9	EKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVREAYSKALFDSVAMQYN	
Q39639	EKRVISFNGTGLSVGPEISFDEIAASRDNPDEVREAYSKALYDSVAKQYN	
Q9FEQ0	EKRVISFNGVGLSLAPAISFEAIAATHRNPDEAREAYSKALFDSVSMQYN	
Q9M4V1	ERRTISFHGVGLSVAPELNFNELTAGCETPEEAKEAFSQALYNSVGEQYN	
SEQ ID NO: 23	

	451	476
P10349	VLKTAISGKQGLGASTADVLSQPW.	
Q9FEP9	VLKTAISGKQGLGASTADVLSQPW.	
Q39639	VLKAAIDGKQELEASVADVLSQPWI	
Q9FEQ0	VLKAAIYGRQALRASTADVLSQPWI	
Q9M4V1	VLKSAIHEHRGLNASNSIISLSQPWQ	
SEQ ID NO: 23	

23/37

Figure 17: Alignment of SEQ ID NO: 27 with Swiss Prot database

	1	50
SEQ ID NO: 27	MEGGGSIIALPLGLMFLFSGFFINILQLLSVLFILPFSRRAYRVVNMIMM	
Q9XFW4	.MAMAAVIVPLGILFFISGLVFNLLQAVCYVLRPMSKNTYRKINRVVA	
Q40119	MAIPAAAFIVPISLLFFMSGLVFNFIQAVFYVLRPISKDTYRRINTLVA	
Q9SDN3	
Q41745	MAIPLVLVPLPLGLLFLLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLA	
Q9SYC8	MKIPAAALVFIPVGVLFLLISGLIVNIIQLVFFIIVRPFSRSLYRRINKNVA	
	51	100
SEQ ID NO: 27	EVLWSELIWLLDWWANVKVKVYTPKESWEHLGKEHALLICNHRSDIDWL	
Q9XFW4	ETLWLELVWIVDWWAGVKIQVFADDETFNRMGKEHALVVCNHRSDIDWL	
Q40119	ELLWLELVWVIDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLI	
Q9SDN3MGKEHALVISNHRSDIDWL	
Q41745	ELLWLQLVWVVDWWAGVKVQLHADEETYRSMGKEHALIISNHRSDIDWLI	
Q9SYC8	ELLWLQLIWLFDDWWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLI	
	101	150
SEQ ID NO: 27	GWIIAQRLGCLGGTRAVMKKSTKFLPVIGWSMWFSEYVFLSRDWAKDEK	
Q9XFW4	GWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYLFERNWAKDEST	
Q40119	GWVLAQRCGCLSSSIAMVKKSSKFLPVIGWSMWFSEYLFERNWAKDENT	
Q9SDN3	GWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWFSEYLFERSWAKDEGT	
Q41745	GWILAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFERSWAKDEKT	
Q9SYC8	GWVMAQRVGCLGSSLAIMKKEAKYLPPIIGWSMWFSDYIFLERSWAKDENT	
	151	200
SEQ ID NO: 27	LKNGYSSLKGFPRTLWVALFVEGTRFTKAKLEAAQKFAADTGLRVPRHVL	
Q9XFW4	LQSGQLQLNDFFRPFWLALFVEGTRFTEAKLAAQEYAASSELVPRNVL	
Q40119	LKSGQLQLNDFFPKPFWLALFVEGTRFTKAKLLAAQEYAASAGLPVPRNVL	
Q9SDN3	LKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAAQEYAAATGLPVPRNVL	
Q41745	LKWGLQRLKDFRPFWLALFVEGTRFTPAKLLAAQEYAASQGLPAPRNVL	
Q9SYC8	LKAGFKRLEDFPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSPRNVL	
	201	250
SEQ ID NO: 27	VPRTKGFVSAVENLREFVPVYDMTVAISKELPNPTMIRIFRGQPSVVHV	
Q9XFW4	IPRTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPPPTMLRLFKGQPSVVHV	
Q40119	IPRTKGFVSAVSNMRSFVPAIYDLTVAIPKTTEQPTMLRLFRGKSSVVHV	
Q9SDN3	IPRTKGFVTAVSQMRSFAPAIYDVTVAIPKSSPAPTMLRLFEGRPSVVHV	
Q41745	IPRTKGFVSAVSIMRDFVPAIYDVTIVPKDSPQPTMLRILKGQSSVIHV	
Q9SYC8	IPRTKGFVSAVSEIRSFVPAIYDCTLTVHNNQPTPTLLRMFSGQSSEINL	

24/37

	251	300
SEQ ID NO: 27	HVRRVPMSDLPEGANAISKWCHDAFHKDDRLEQHEKENTFGEDLYIPIE	
Q9XFW4	HIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDKHIAADTFPGQKEQNIG	
Q40119	HLKRHLMKDLPKTDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVQDIG	
Q9SDN3	HIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDKHTVEQTFGDQQLKVTG	
Q41745	RMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTFD.EEIRPIG	
Q9SYC8	QMRRHKMSELPEITDDGIAQWCQDLFITKDAQLEKYFTKDVFSDELVHQIN	

	301	350
SEQ ID NO: 27	RPLKPLIIVISWAITLLAAAWFLRR..VLSTWKGIWVAGVLVVMLCV	
Q9XFW4	RPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCM	
Q40119	RPMKSLVVVSWMCLLCLGLVKFLQWSALLSSWKGMITTFVLGIVTVLM	
Q9SDN3	RPLKSLLVVTAWACLLILGALKFLYWSSLLSSWKGIAFSALGLGVTVLM	
Q41745	RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVM	
Q9SYC8	RPIKPLIVVIIWLGLVFGGFKLLQWLSIVASWKIILLFVFFLVIATITM	

	351	391
SEQ ID NO: 27	QILVMSSQSERSSDPAAKKANQKQAASVAHLGKTD.....	
Q9XFW4	QILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK	
Q40119	HILIRSSQSEHSTPAKTRARQTAENPK.....	
Q9SDN3	QILIRFSQSERSTPAPVAPTNNKNKGESSGKPEKQQ.....	
Q41745	HVFIMFSQAERSSSARAARNRVKKE.....	
Q9SYC8	QILIQSSESQRSTPAKRPLQEQLISA.....	

25/37

Figure 18: Alignment of SEQ ID NO: 8 with Swiss Prot database

	1	50
SEQ ID NO: 8	MESTADVGMSSDDDPILLNGLETPLLAEFPLGERPTIGPEAPVNPFPHEPDG	
P42322	
Q9NKW7	
Q9XFJ4MGQREDIRTLSENEYETDIPRRGGLSVVRGTRRRRTLHSGQHHE	
O35259	
Q9FF57	
	51	100
SEQ ID NO: 8	GWKTNNNEWNYFQMMKSILLIPLLLVRLVSMITIVAFGYVWIRICLIGVTD	
P42322	
Q9NKW7	
Q9XFJ4	VVAIKTLR.RFGPPPAPEKKS LNKS RVPQAAL ISETLLTNELLVMIKIVE	
O35259METIMDDEVTKRTSAEELESWNLLSRTNYN.	
Q9FF57MIEQLGLIIIMGLIHYQSERVKPREWLKLSSSENSR	
	101	150
SEQ ID NO: 8	PLFKPFNPCRRLWGIRLVARAVMFTMGYYYIPIKGPAPHRSEAPIIVS	
P42322	
Q9NKW7	
Q9XFJ4	DVSPHPNVIHLYDVCEDPSGVHLILELCSGGELFDRIAGQARYNEEGAAA	
O35259	...FQYISLRLTILWGLGVLRICYFLPLRLALFTGIGLLVVGTTMVG	
Q9FF57	LG.NTKTNHRRSFTGDVSYEQRDLLDISPTLTEAAGAI VDFHCFKTCRCF	
	151	200
SEQ ID NO: 8	NHIGFLDPIFVFYRHLPAIVSAKENVEMPIIGLFLQALQIIPVDRDQAQS	
P42322	
Q9NKW7	
Q9XFJ4	VVRQIAKGLEALHGASIVHRDLKPENCLFLNKDENSPLKIMDFGLSSIED	
O35259	LPNGRFKEFLSKHVHLMCYR.....	
Q9FF57	TLAFGWIIIFLSLFIPVNALLK.....	
	201	250
SEQ ID NO: 8	RHHAAGNVRRRAVDNMWVSHVMLFPQGT TTNGRAIIAFKTGAFSPGLPVQP	
P42322	
Q9NKW7	
Q9XFJ4	FANPVVGLFGSIDYVSPEALSREKITT KSDIWSLGVILYILLSGYPPFIA	
O35259	
Q9FF57GQDRLRKKIER	

26/37

	251	300
SEQ ID NO: 8	MVIRYPHKYVNPSCWDQGGPLVVVLQLMTQFINHMEVEYLPVMKPTVREM	
P42322	
Q9NKW7	
Q9XFJ4	PSNRQKQQMILNGQFSFDEKWTWKNISSSAKQLISSLLKVDPNMRPTAQEI	
O35259	ICVR.ALTAIITYHN.....	
Q9FF57	VLVEMICSFFVASWTG.....	
	301	350
SEQ ID NO: 8	KYPHEFASVRSEMAKALGIVCTEHSFLD...IKLALAAEKLKQPSGRSL	
P42322MGTNTSSLRP	
Q9NKW7MGN	
Q9XFJ4	LEHPWVTGDLAKQEQMDAEIVSRLQSFNARRKFRAAAMASILSSSFSLRT	
O35259RKNRPRN.....GG	
Q9FF57VVKYHGPRPSIRP...KQ	
	351	400
SEQ ID NO: 8	VEFARMEKLFRLDFPTAKEYLEKFSAMDRTHSGF..VTFEELCTALDLP.	
P42322	EEVEEMQKGTNFTQKEIKKLYKRFFKKLDKDGNGT..ISKDEFLMIPELA.	
Q9NKW7	ENSLPMELC SNFDPDEIKRLGKRFRKLDLDNSGS..LSVDEFMTLPQL.	
Q9XFJ4	KKLKKLVGSYDLKPEELENLSHNFKKICKNGENSTLLEFEEVLKAMEMSS	
O35259	ICVANHTSRIDVIIIFASDGYIAMVGQVHGGLMGVIQRAMVKACPHVWFE.	
Q9FF57	VYVANHTSMIDFIVLEQMTAFVIMQKHGPGWVGLLQSTILESVCIWFN.	
	401	450
SEQ ID NO: 8	RSPITKQVFNLFDKDGHSINFRFLAGLAFVSSHTSFSSTMEAAFKACD	
P42322	VNPLVKRVISIFDENGDSVNFKEFIAALSVFNAQGDQQRKLEFAFKVYD	
Q9NKW7	QNPLVQRVIDIFD TDNGEVD FKEFIEGVSQFSVKGDKLSKLRFAFKIYD	
Q9XFJ4	LVPLAPRIFDLFDNNRDGTVDMRIIGGFSSLKYSQGD.DALRLCFQVYD	
O35259	RSEVKDRHLVAKRLTEHVQDKSKLPILIFPEGTCINNT.SVMMFKKGSFE	
Q9FF57	RSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVNNN.YTVMFKKGAFE	
	451	500
SEQ ID NO: 8	VNGDGTLSRDEVERSLLDIFPELPPI.....TVFKLFDTLINHDEKIS	
P42322	IDGDGYISNGELFTVLKMMVGNNLSD.VQLQQIVDKTILEADEDGDGKIS	
Q9NKW7	MDKDGYSNGELFQVLKMMVGNNLKD.TQLQQIVDKTIIHADADGDGKIS	
Q9XFJ4	TDRSGCISKEEVESMLRALPEDCLPINITEPGKLDEIFDLMDANS DGKVT	
O35259	IGATVYPVAIKYDPQFGDAFWNSSKYG.....MVTYLLRMMTSWAIVCSV	
Q9FF57	LDCTVCPIAIKYNKIFVDAFWNSRKQS.....FTMHLLQLMTSWAVVCEV	

27/37

	501	550
SEQ ID NO: 8	WEEFSSFLQRNPEYLAIIIYAHPTLLKPPTSTS.....	
P42322	FEEFAKTLSHQDLENKMTIRL.....	
Q9NKW7	FEEFCAVVGNMVDVHKKMVVDV.....	
Q9XFJ4	FDEFKAAMQRDSSLQDVVLSSLRPN.....	
O35259	WYLPPMTREKDEDAVQFANRVKSAIARQEDW.....	
Q9FF57	WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHS	

	551	568
SEQ ID NO: 8	
P42322	
Q9NKW7	
Q9XFJ4	
O35259	
Q9FF57	ERKQQSFAESILARLEEK	

28/37

Figure 19: Alignment of SEQ ID NO: 10 with Swiss Prot database

	1	50
Q24214	
P28470	
SEQ ID NO: 10	MTSTENTAMFTEDTSTLNGSTEANHAEFPLGERPTIGPEPPVNPFHESST	
O35259METIMDDEVTKRTSAEEL	
Q9XFJ4	MGQREDIRTLSNEYEVTDIPRRGGLSVVRRGTRRRRTLHSGQHHEVVAIKT	
	51	100
Q24214	
P28470	
SEQ ID NO: 10	WSIPQVIKTILLVPLLVIKLLSMFALMMLGYICVKVAMIGCKDPLFKPFN	
O35259	ESWNLLSRTNYNFYISLRLTILWGLGVLIKYCFLLP.....	
Q9XFJ4	LRRFGPPPAPPEKKSLSKSRVPAALISETLLTNELLVMIKIVEDVSPHPN	
	101	150
Q24214	
P28470	
SEQ ID NO: 10	PLRRLLLSVRLIARGVMVAMGYYYILVKGKPAHRSVAPIIVSNHIGFVD	
O35259LRIALFTGIGLLVVG.....TTMVG...	
Q9XFJ4	VIHLYDVCEDPSGVHLILELCSSGELFDRIAGQARYNEEGAAAVVRQIAK	
	151	200
Q24214	
P28470	
SEQ ID NO: 10	PIFVFYRHLPIVIVSAKEIVEMPIIGMFLQALQIIPVDRINPASRHHAAGN	
O35259YLPNGRFKEFLSKH....	
Q9XFJ4	GLEALHGASIVHRDLKPENCLFLNKDENSPLKIMDFGLSSIEDFANPVVG	
	201	250
Q24214	
P28470	
SEQ ID NO: 10	IRRRAMDNEWPHVMLFPEGTTTNGKALISFKTGAFSPGLPVQPMVIKYPH	
O35259VHLMCYR.....	
Q9XFJ4	LFGSIDYVSPEALSREKITTKSDIWSLGVILYILLSGYPPFIAPSNRQKQ	
	251	300
Q24214	
P28470	
SEQ ID NO: 10	KYVNPCWCNQGGPLVILFQLMTQFVNYMEVEYLPVMTPNVHEIKNPHEFA	
O35259ICVR.....ALTAITYHNRK	
Q9XFJ4	QMILNGQFSFDEKTKWNISSSAKQLISSLLKVDPNMRPTAQEILEHPVWT	

29/37

301 350
Q24214MGNETSLPME
P28470GNEASYHSE
SEQ ID NO: 10 NRVRTAKALGVVCTEHNF...LDIKLKMAAEKQPSGRSLVEFARME
O35259 NRPR.....N.....GGICVANHT
Q9XFJ4 GDLAKQEQMDAEIVSRLQSFNARRKFRAAAMASILSSSFSLRTKKLKKLV

351 400
Q24214 MCSNFDADAEIRRLGKRFRKLDLD..NSGALSVDEFMSLPQLQ.QNPLVQR
P28470 MGTHFDHDEIKRLGRSFKKMDLD..KSGSLSVDEFMSLPQLQ.QNPLVGR
SEQ ID NO: 10 KLFRLDYSKAQEYLEKFSAMDPS..HSGYVTYDEFLKALHLP.PTQITEQ
O35259 SRIDVIFASDGYAMVGQVHGG..LMGVIQRAMVKACPHVW.FERSEVK
Q9XFJ4 GSYDLKPEELENLSHNFKKICKNGENSTLLEFEVLKAMEMSSLVPLAPR

401 450
Q24214 VIDIFDADGNGEVDKFQVVSQFS.VKGDKLSKLRFARIYDMDNDGY
P28470 VIDIFDADGNGEVDKFQVVSQFS.VKGDDEQKLRFARIYDMDNDGY
SEQ ID NO: 10 VFNLFDKNGHGSINFREFVAGLAFLS.THTSFQTTMKAAPKACDVGDT
O35259 DRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVY
Q9XFJ4 IFDLFDNNDGTVDREIIGGFSSLK..YSQDDALRLCFQVYDTRSGC

451 500
Q24214 ISNGELFQVLKMMVGNLKD.TQLQQIVDKTIGFADKDEDGKISDFEFC
P28470 ISNGELFQVLKMMVGNLKD.WQLQQLVDKSILVLDKDGGRISFEFRD
SEQ ID NO: 10 LTRNEVESSLMAVFP.....ELPPATVLKLFDTLDLNRDGSINWEEFSS
O35259 PVAIKYDPQFGDAFWN.....SSKYGMVTYLLRMTSWAIVCS
Q9XFJ4 ISKEEVESMLRALPEDCLPINITEPGKLDEIFDLMDANSKGKVTDFEFA

501 532
Q24214 VVGNTDIHKKMVVDV.....
P28470 VVRTMEIHKKLVVFDHGQED.....
SEQ ID NO: 10 FLQRNPEYLAIILAAHPTLLQAPKSESEETNI
O35259 VWYLPMTREKDEDAVQFANRVKSAIARQEDW
Q9XFJ4 AMQRDSSLQDVVLSLRPN.....

30/37

Figure 20: Alignment of SEQ ID NO: 12 with Swiss Prot database

	1	50
Q9XFW4	.MAMAAVIVPLGILFFISGLVNNLLQAVCYLVRPMSKNTYRKINRVVA	
Q9SDN3	
Q40119	MAIPAAAFIVPISLLFFMSGVLVNFQAVFYVLRPISKDTYRRINTLVA	
Q41745	MAIPLVLVVLPLGLLFLLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLA	
Q9SYC8	MKIPAALVFIPVGVLFLLISGLIVNIIQLVFFIIVRPFSRSLYRRINKNVA	
SEQ ID NO: 12MIMM	
	51	100
Q9XFW4	ETLWLELVWIVDWWAGVKIQVFADDETFNRMGKEHALVVCNHRSDIDWL	
Q9SDN3MGKEHALVISNHRSDIDWL	
Q40119	ELLWLELVWVIDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLI	
Q41745	ELLWLQLVWVVDWWAGVKVQLHADEETYSRSMGKEHALIISNHRSDIDWLI	
Q9SYC8	ELLWLQLIWLFDWWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLI	
SEQ ID NO: 12	EVLWSELIWLLDWWANVKVKVYTPKESWEHLGKEHALLICNHRSDIDWL	
	101	150
Q9XFW4	GWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYFLERNWAKDEST	
Q9SDN3	GWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWFSEYFLERSWAKDEGT	
Q40119	GWVLAQRSGCLSSSIAMKKSSKFLPVIGWSMWFSEYFLERNWAKDENT	
Q41745	GWILAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYFLERSWAKDEKT	
Q9SYC8	GWVMAQVRGCLGSSLAIMKKEAKYLPPIGWWSMWFSDYIFLERSWAKDENT	
SEQ ID NO: 12	GWIIAQRGCLGGTRAVMKKSTKFLPVIGWSMWFSEYVFLSRDWAKDEKV	
	151	200
Q9XFW4	LQSGLQRLNDFPRPFWLALFVEGTRFTTEAKLKAAQEYAAASSELVPRNV	
Q9SDN3	LKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAAQEYAAATGLVPRNV	
Q40119	LKSGLQRLNDFPKPFWLALFVEGTRFTKAKLLAAQEYAAASAGLVPRNV	
Q41745	LKWGLQRLKDFPRPFWLALFVEGTRFTPAKLLAAQEYAAASQGLPAPRV	
Q9SYC8	LKAGFKRLEDPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSPRV	
SEQ ID NO: 12	LKNGYSSLKGFPRTLWVLFVEGTRFTKAKLEVAQKFAADTGLRVPRV	
	201	250
Q9XFW4	IPRTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPPPTMLRLFKGQPSVVHV	
Q9SDN3	IPRTKGFVTAVSQMRSFAPAIYDVTVAIPKSSPAPTMLRLFEGRPVVHV	
Q40119	IPRTKGFVSAVSNMRSFVPAIYDLTVAIPKTTEQPTMLRLFRGKSSVVHV	
Q41745	IPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRILKGQSSVIHV	
Q9SYC8	IPRTKGFVSAVSEIRSFVPAIYDCTLTVHNNQPTPTLLRMFSGQSSEINL	
SEQ ID NO: 12	VPRTKGFVSAVENLREFVPVYDMTVAISKELPNPTMIRIFRGQPSVVHV	

31/37

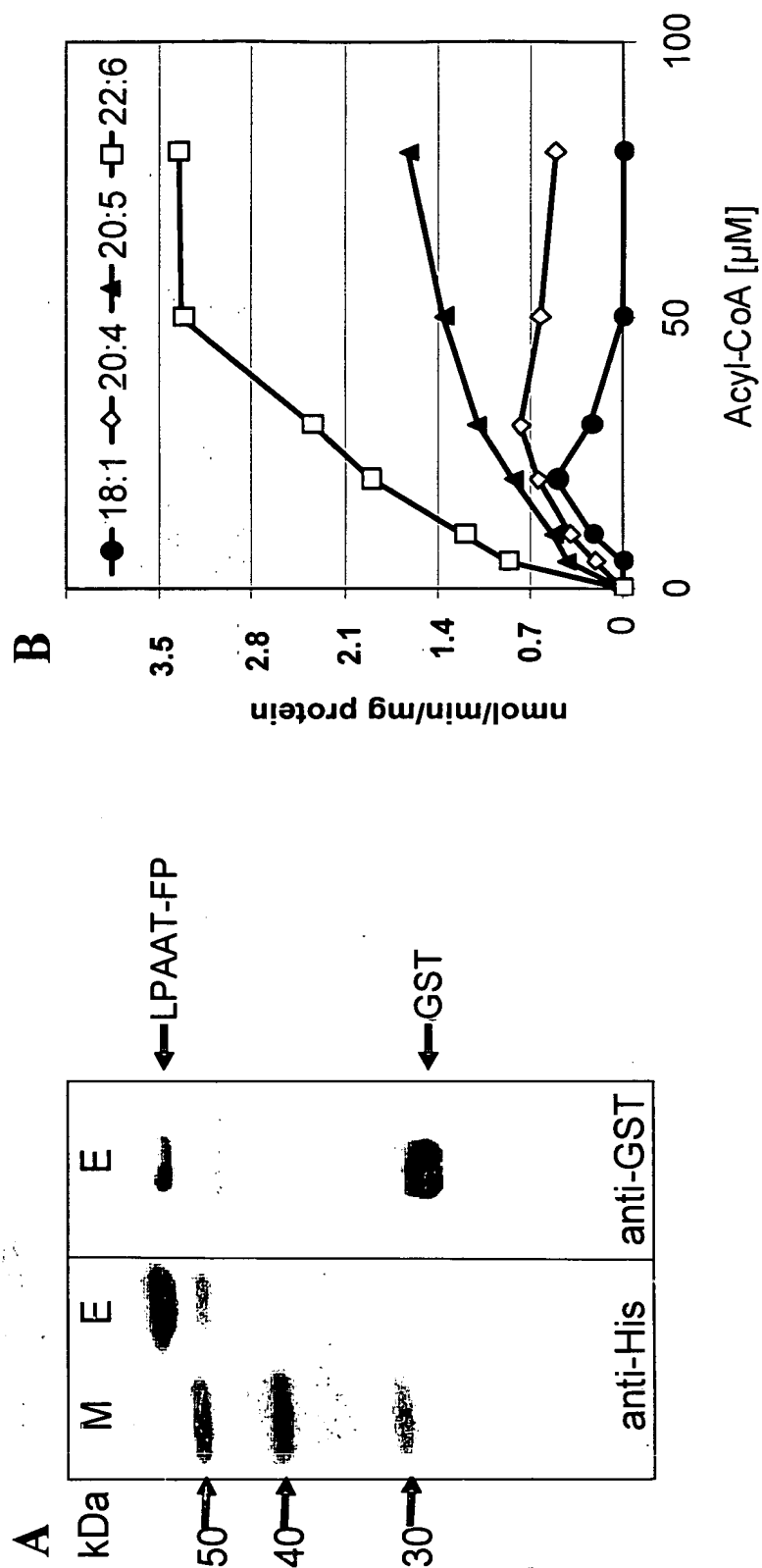
	251	300
Q9XFW4	HIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDKHIAADTFPGQKEQNIG	
Q9SDN3	HIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDKHTVEQTFGDQQLKVTG	
Q40119	HLKRHLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVQDIG	
Q41745	RMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTFD.EEIRPIG	
Q9SYC8	QMRRHKMSELPETDDGIAQWCQDLFITKDAQLEKYFTKDVFSDLVHQIN	
SEQ ID NO: 12	YVRRVPMSDLPEGANAISKWCHDAFHKDDRLEQHEKENTFGEDLYPIE	

	301	350
Q9XFW4	RPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCM	
Q9SDN3	RPLKSLLVVTAWACLLILGALKFLYWSSLLSSWKGIASFALGLGVTVLM	
Q40119	RPMKSLVVVSWMCLLCLGLVKFLQWSALLSSWKGMITTFVLGIVTVLM	
Q41745	RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVM	
Q9SYC8	RPIKPLIVVIIWLGLVFGGFKLLQWLSIVASWKIILLFVFFLVIATITM	
SEQ ID NO: 12	RPLKPLIIVISWAITLLAAAWFLRR.VLSTWKGIWVAGVLVVMLCV	

	351	391
Q9XFW4	QILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK	
Q9SDN3	QILIRFSQSERSTPAPVAPTNNKNKGESSGKPEKQQ.....	
Q40119	HILIRSSQSEHSTPAKTRARQTAENPK.....	
Q41745	HVFIMFSQAERSSSARAARNRVKKE.....	
Q9SYC8	QILIQSSESQRSTPAKRPLQEQLISA.....	
SEQ ID NO: 12	QILVMSSQSERSSDPAKKANQKQAASVAHLGKTD.....	

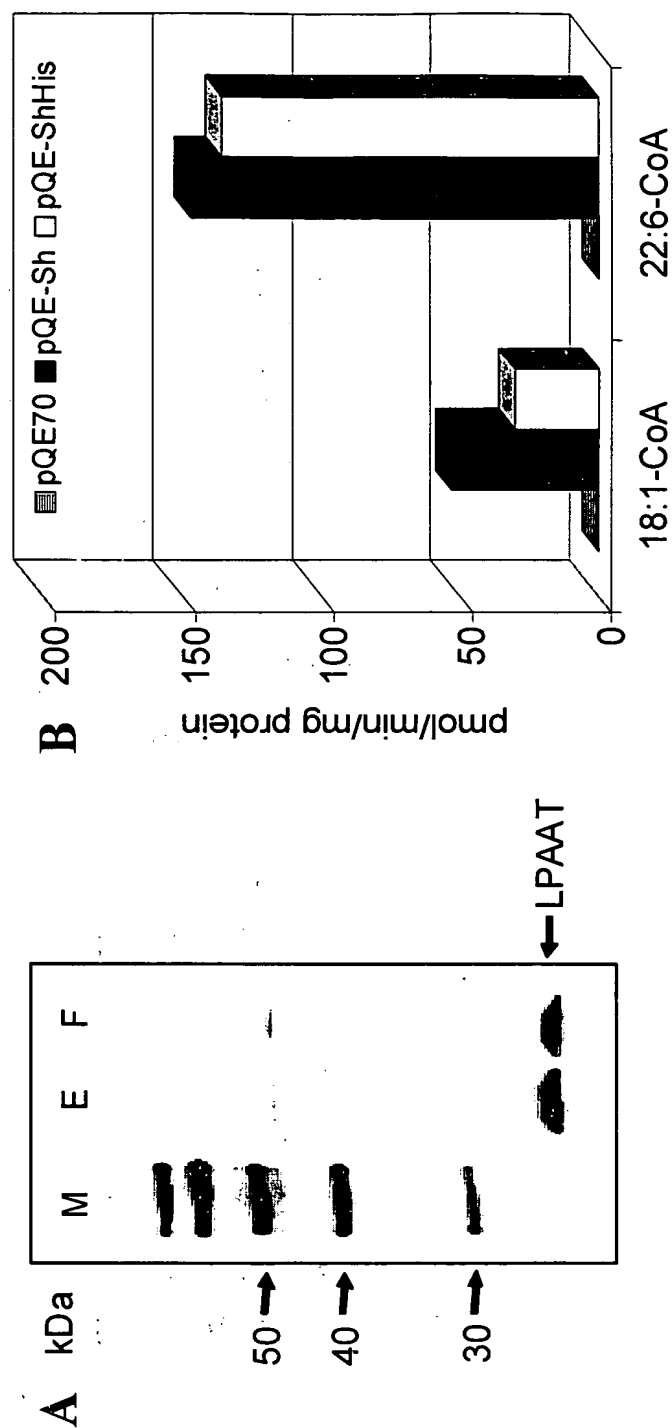
Figure 21: **A.** Western blot analyses of the *Thraustochytrium* LPAAT expressed in *E. coli* as fusion protein (LPAAT-FP) with N-terminal GST tag and C-terminal His tag.

B Acyl-CoA specificity of the *Thraustochytrium* LPAAT expressed as GST fusion protein in *E. coli*

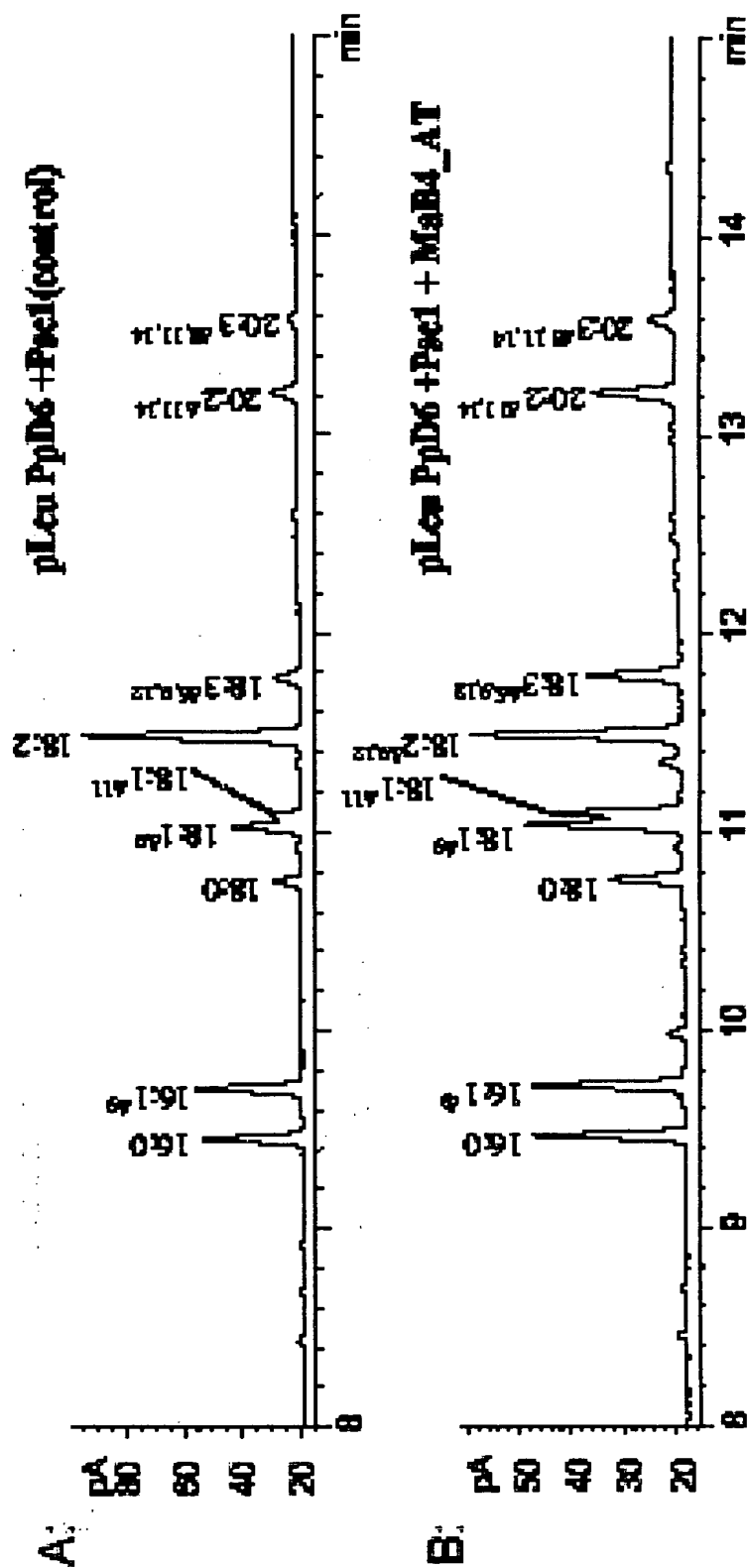


33/37

Figure 22: A: Western blot analysis of the *Shewanella* LPAAT expressed in *E. coli* as fusion protein with C-terminal His tag. B: Functional expression of the *Shewanella* LPAAT in *E. coli*



34/37

Figure 23: Expression of Mortierella LPAAT (MaB4_AT) in yeast, and feeding of 18:2 Δ 9,12 fatty acids (A + B)

35/37

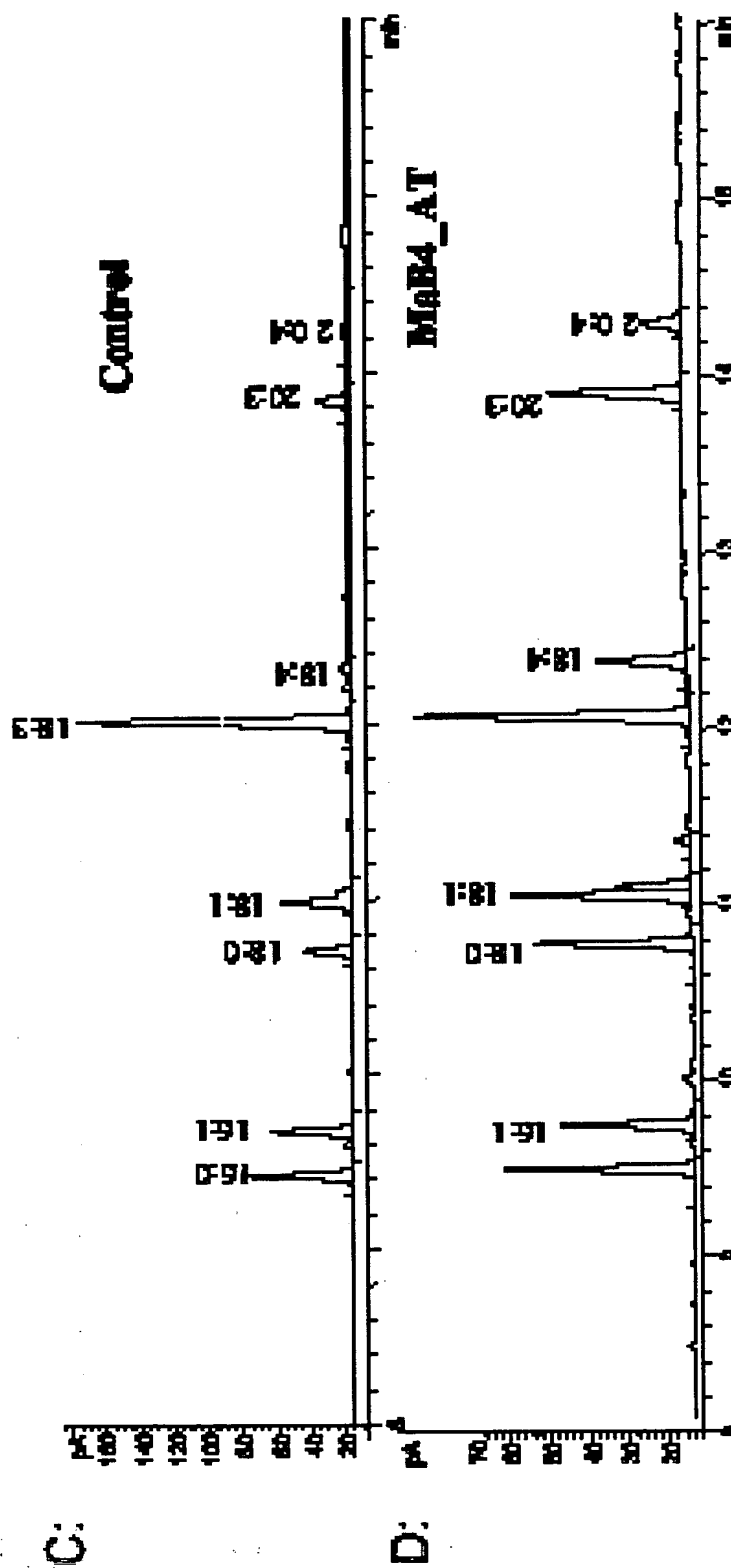
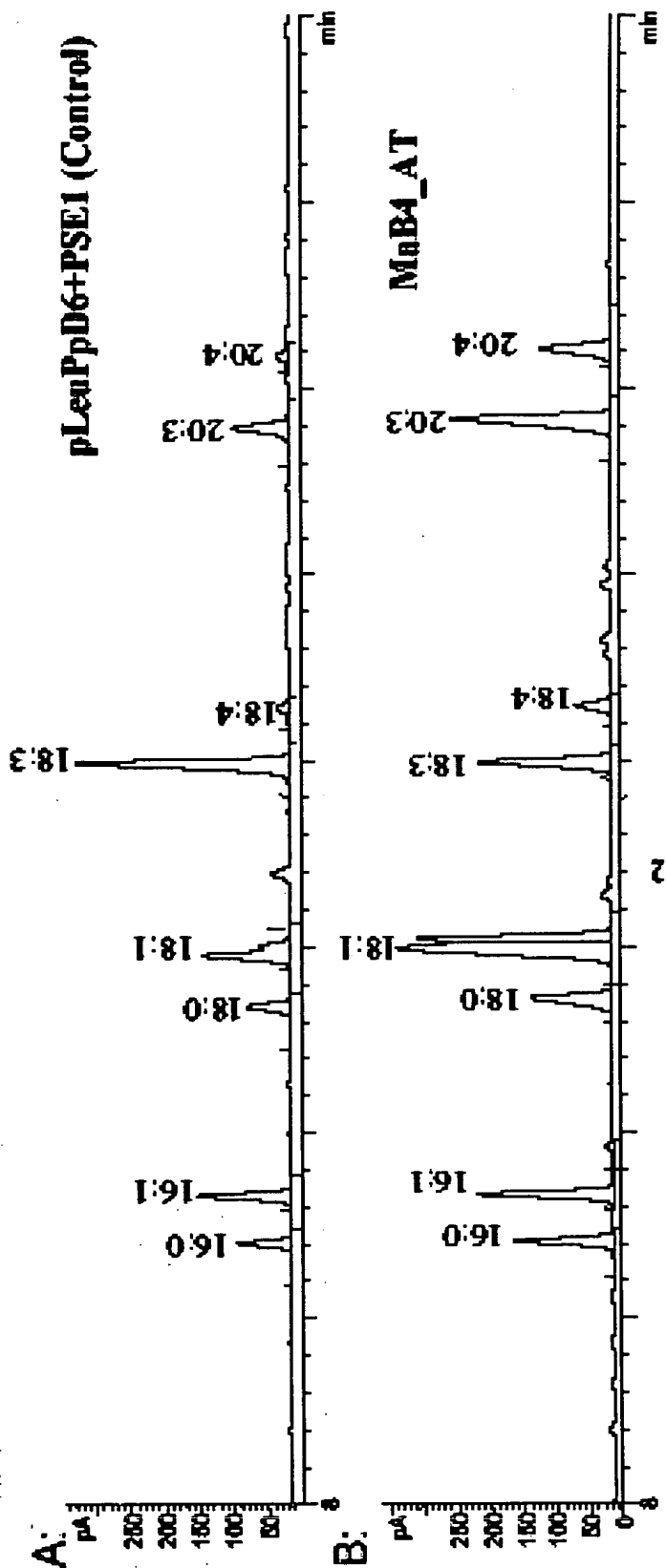


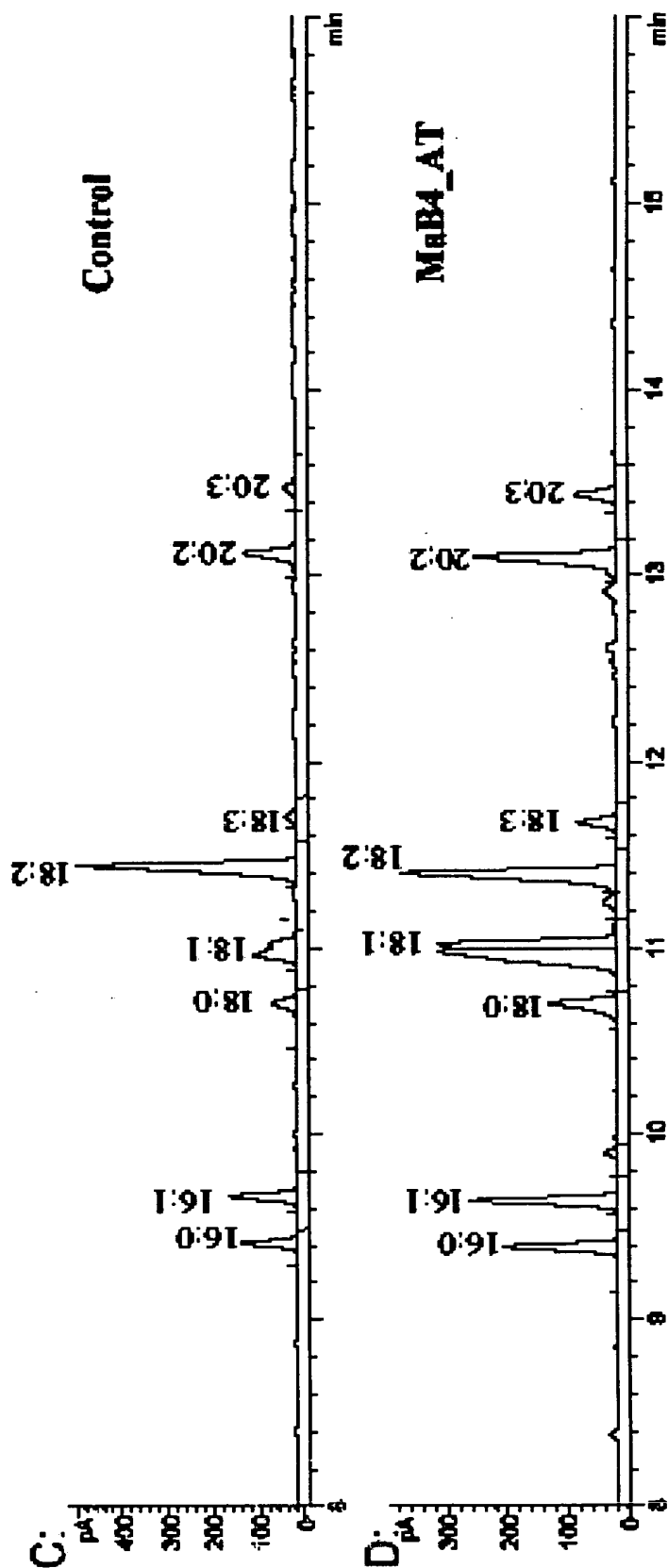
Figure 24: Expression of Mortierella LPAAT (MaB4_AT) in yeast, and feeding of 18:3 Δ 9,12,15 fatty acids (C + D)

Figure 25: Expression of Mortierella LPAAT (MaB4_AT) in yeast, and feeding of 18:2 Δ 9,12 fatty acids (A + B). Analysis of the neutral lipids.



37/37

Figure 26: Expression of Mortierella LPAAT (MaB4_AT) in yeast, and feeding of 18:3 Δ 9,12,15 fatty acids (C + D). Analysis of the neutral lipids.



This Page is inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ BLACK BORDERS
- ☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLORED OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REPERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images
problems checked, please do not report the
problems to the IFW Image Problem Mailbox**